



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 100977

TO: Elizabeth Kemmerer
Location: CM1/10B17/10D19
Art Unit: 1646
Tuesday, August 19, 2003
Case Serial Number: 09581252

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Kemmerer,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(703)305-1954



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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 14:30:54 ; Search time 83 Seconds

(without alignments)
675,066 Million cell updates/sec

Title: US-09-581-252-14

Perfect score: 1848
Sequence: 1 MNECHYKHMDFYNSRMTD.....GSQYIEDISOGAVCNKSTS 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Minimum number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq.19Jun03.*

1: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	353	20	AAV24240
2	1838	99.5	353	20	AAV24241
3	1838	99.5	353	21	AAV24242
4	1838	99.5	353	21	AAV24243
5	1838	99.5	353	22	AAV24244
6	1838	99.5	353	23	AAV24245
7	1838	99.5	353	23	AAV24246
8	1838	99.5	353	24	AAV24247
9	1838	99.5	353	24	AAV24248

10	1838	99.5	353	24	ABU56733
11	1838	99.5	353	24	ABU56734
12	1838	99.5	353	24	ABU56735
13	1775	96.0	353	24	ABU56736
14	1772.5	95.9	354	21	ABU56737
15	1697.5	91.9	354	24	ABU56738
16	1692.5	91.6	354	24	ABU56739
17	1692.5	91.6	354	21	ABU56740
18	1692.5	91.6	354	23	ABU56741
19	1682.5	91.0	354	24	ABU56742
20	1642.5	88.9	345	24	ABU56743
21	1546	83.7	338	19	AAU56801
22	1014.5	54.9	220	22	AAU56802
23	995	53.8	213	20	AAV24244
24	948.5	51.3	364	18	AAU56819
25	948.5	51.3	364	20	AAU56820
26	948.5	51.3	364	22	AAU56821
27	948.5	51.3	364	22	AAU56822
28	948.5	51.3	364	24	ABU56823
29	948.5	51.3	364	24	ABU56824
30	948.5	51.3	364	24	ABU56825
31	946.5	51.2	364	19	AAU56826
32	946.5	51.2	364	19	AAU56827
33	946.5	51.2	364	20	AAU56828
34	946.5	51.2	364	20	AAU56829
35	944.5	51.1	364	18	AAU56830
36	853.5	46.2	351	20	AAU56831
37	849.5	46.0	348	23	ABU56832
38	849.5	46.0	382	20	AAU56833
39	849.5	46.0	382	21	AAU56834
40	849.5	46.0	382	22	AAU56835
41	849.5	46.0	382	24	ABU56836
42	849.5	46.0	382	24	ABU56837
43	843.5	45.6	351	19	AAU56838
44	843.5	45.6	351	21	AAU56839
45	843.5	45.6	351	23	AAU56840

ALIGNMENTS

RESULT 1	AAV24240	standard; Protein; 353 AA.
ID	AAV24240	
XX	AAV24240	
AC	AAV24240	
XX	13-SEP-1999	(first entry)
XX		
DE	Human EDG-5 receptor.	
XX		
KW	EDG-5; HEDG-5; MEGD-5; receptor homologue; asthma; rheumatoid arthritis;	
KW	adult respiratory distress syndrome; cardiac ischaemia; septic shock;	
KW	acute pancreatitis; psoriasis; acute cyclosporine nephrotoxicity;	
KW	early diabetic glomerulopathy; lung damage.	
XX		
OS	Homo sapiens.	
XX		
PN	WO933972-A1.	
XX		
PD	08-JUL-1999.	
XX		
PF	24-DEC-1998;	98MO-CA01193.
XX		
PR	24-DEC-1997;	97US-0997803.
XX		
PA	(ALIX) ALLELIX BIOPHARMACEUTICALS INC.	
XX		
PI	Chun JW, Gupta AK, Munroe DG, Vyas TB;	
XX		
DR	WPI; 1999-419106/35.	
DR	N-PSDB; AAX88745.	
XX		

PT Nucleotide sequences encoding mammalian EDG-5 receptors
XX
XX
PS Claim 13; Fig 4A; 87pp; English.
CC The present sequence is a human EDG-5 (HEDG-5) receptor homologue.
CC EDG-5 sequences may be used to test for aberrant expression of HEDG-5
CC and can accelerate diagnosis and proper treatment of conditions such as
CC adult respiratory distress syndrome, asthma, rheumatoid arthritis,
CC cardiac ischaemia, acute pancreatitis, septic shock, psoriasis, acute
CC cyclosporine nephrotoxicity and early diabetic glomerulopathy, as well
CC as lung damage following exposure to cigarette smoke, asbestos, or
CC silica. HEDG-5 specific antibodies, inhibitors and ligands may be used
CC to treat inflammation or diseases including, viral, bacterial or fungal
CC infections, allergic responses, mechanical injury associated with
CC trauma, hereditary diseases, lymphoma or carcinoma, or other conditions
CC which activate the genes of kidney, lung, heart, lymphoid or tissues of
CC the nervous system.
XX
SQ Sequence 353 AA;
Query Match 100.0%; Score 1848; DB 20; Length 353;
Best Local Similarity 100.0%; Pred. No. 2.3e-197;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MNECHYKHMDFEYRNSNTDVTDMGTGKLYIVLCVGFECLEFFFSNSLYIAVINKRK 60
1 MNECHYKHMDFEYRNSNTDVTDMGTGKLYIVLCVGFECLEFFFSNSLYIAVINKRK 60
QY 61 FHFFPYLLANLAADFPAGIAYVFLMFGNPGVSKTTLVNMFLRQGLDSSLTASLTNL 120
61 FHFFPYLLANLAADFPAGIAYVFLMFGNPGVSKTTLVNMFLRQGLDSSLTASLTNL 120
DB 121 LVIAVERHMSIMRRVNSNLTGKRVTLILLVMAIAIFMGAVPTLGNMCLNISACSSLA 180
121 LVIAVERHMSIMRRVNSNLTGKRVTLILLVMAIAIFMGAVPTLGNMCLNISACSSLA 180
QY 181 PIYSRSLVFWTWSNLAFLIMVYVLRITYYVARKTNVLSPHSGSISRRTPMKLMKT 240
181 PIYSRSLVFWTWSNLAFLIMVYVLRITYYVARKTNVLSPHSGSISRRTPMKLMKT 240
DB 241 VMTVLGAFVVCWMTGGLVLLPLDGLNCRCQGVQVHKRKFLLALLNSVNPPIIYSYKDEDM 300
241 VMTVLGAFVVCWMTGGLVLLPLDGLNCRCQGVQVHKRKFLLALLNSVNPPIIYSYKDEDM 300
QY 301 YGTMKKMICPSQENPERRPSRIPSTVLSRSDTSQYIEDSISOGAVCNKSTS 353
301 YGTMKKMICPSQENPERRPSRIPSTVLSRSDTSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKKMICPSQENPERRPSRIPSTVLSRSDTSQYIEDSISOGAVCNKSTS 353
RESULT 2
ID AAY24241 standard; Protein: 353 AA.
AC AAY24241;
XX
DT 13-SEP-1999 (first entry)
XX
DE Human EDG-5 receptor clone pc3-hedg5#3.4 protein.
XX
KW EDG-5; HEDG-5; MEDG-5; receptor homologue; asthma; rheumatoid arthritis;
KW adult respiratory distress syndrome; cardiac ischaemia; septic shock;
KW acute pancreatitis; psoriasis; acute cyclosporine nephrotoxicity;
KW early diabetic glomerulopathy; lung damage.
OS
XX Homo sapiens.
XX
PN WO9933972-A1.
XX
PD 08-JUL-1999.
XX
PF 24-DEC-1998; 98WO-CA01193.
XX
PR 24-DEC-1997; 97US-0997803.

XX
PA (ALIX) ALLELIX BIOPHARMACEUTICALS INC.
XX
XX Chun JYM, Gupta AK, Munroe DG, Vyas TB;
PI
XX WPI: 1999-419106/35.
DR
XX N-PSDB: AAX86746.
PT Nucleotide sequences encoding mammalian EDG-5 receptors
PS Claim 13; Fig 4B; 87pp; English.
XX
XX
CC The present sequence is a human EDG-5 (HEDG-5) receptor homologue.
CC EDG-5 sequences may be used to test for aberrant expression of HEDG-5
CC and can accelerate diagnosis and proper treatment of conditions such as
CC adult respiratory distress syndrome, asthma, rheumatoid arthritis,
CC cardiac ischaemia, acute pancreatitis, septic shock, psoriasis, acute
CC cyclosporine nephrotoxicity and early diabetic glomerulopathy, as well
CC as lung damage following exposure to cigarette smoke, asbestos, or
CC silica. HEDG-5 specific antibodies, inhibitors and ligands may be used
CC to treat inflammation or diseases including, viral, bacterial or fungal
CC infections, allergic responses, mechanical injury associated with
CC trauma, hereditary diseases, lymphoma or carcinoma, or other conditions
CC which activate the genes of kidney, lung, heart, lymphoid or tissues of
CC the nervous system.
XX
SQ Sequence 353 AA;
Query Match 99.5%; Score 1838; DB 20; Length 353;
Best Local Similarity 99.7%; Pred. No. 3.1e-196;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 MNECHYKHMDFEYRNSNTDVTDMGTGKLYIVLCVGFECLEFFFSNSLYIAVINKRK 60
1 MNECHYKHMDFEYRNSNTDVTDMGTGKLYIVLCVGFECLEFFFSNSLYIAVINKRK 60
QY 61 FHFFPYLLANLAADFPAGIAYVFLMFGNPGVSKTTLVNMFLRQGLDSSLTASLTNL 120
61 FHFFPYLLANLAADFPAGIAYVFLMFGNPGVSKTTLVNMFLRQGLDSSLTASLTNL 120
DB 121 LVIAVERHMSIMRRVNSNLTGKRVTLILLVMAIAIFMGAVPTLGNMCLNISACSSLA 180
121 LVIAVERHMSIMRRVNSNLTGKRVTLILLVMAIAIFMGAVPTLGNMCLNISACSSLA 180
QY 181 PIYSRSLVFWTWSNLAFLIMVYVLRITYYVARKTNVLSPHSGSISRRTPMKLMKT 240
181 PIYSRSLVFWTWSNLAFLIMVYVLRITYYVARKTNVLSPHSGSISRRTPMKLMKT 240
DB 241 VMTVLGAFVVCWMTGGLVLLPLDGLNCRCQGVQVHKRKFLLALLNSVNPPIIYSYKDEDM 300
241 VMTVLGAFVVCWMTGGLVLLPLDGLNCRCQGVQVHKRKFLLALLNSVNPPIIYSYKDEDM 300
QY 301 YGTMKKMICPSQENPERRPSRIPSTVLSRSDTSQYIEDSISOGAVCNKSTS 353
301 YGTMKKMICPSQENPERRPSRIPSTVLSRSDTSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKKMICPSQENPERRPSRIPSTVLSRSDTSQYIEDSISOGAVCNKSTS 353
RESULT 3
ID AAB10098 standard; Protein: 353 AA.
AC AAB10098;
XX
DT 10-NOV-2000 (first entry)
XX
DE Human G protein-coupled receptor hAL7T024.
XX
KW G protein-coupled receptor; AL7T024; treatment; prevention; diagnosis;
KW nervous system disorder; Alzheimer's disease; dementia; hypertension;
KW inflammatory disorder; allergy; rheumatism; asthma; arteriosclerosis;
KW cardiovascular disorder; cancer; human.
OS
XX Homo sapiens.

XX WO200035953-A1.
XX 22-JUN-2000.
XX 09-DEC-1999; 99WO-JP06904.
XX 11-DEC-1998; 98JP-0353165.
XX 08-FEB-1999; 99JP-0029677.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Watanabe T, Kikuchi K, Shintani Y;
XX WPI; 2000-442368/38.
XX N-PSDB; AAA40370.
XX G-protein coupled receptor protein and antibodies to it for treatment
XX and diagnosis of nervous system, inflammatory and other disorders
XX
XX Claim 2; Page 88-90; 94pp; Japanese.

CC This invention describes a novel G-protein coupled receptor protein
CC (AL7T024) and its salts. The products of the invention can be used for
CC the treatment, prevention and diagnosis of diseases with which the
CC receptor protein is associated, including nervous system disorders (such
CC as Alzheimer's disease and dementia), inflammatory disorders (such as
CC allergies, rheumatism and asthma), cardiovascular disorders (such as
CC hypertension and arteriosclerosis), and cancer. This sequence represents
CC the human G protein-coupled receptor protein which is described in the
CC method of the invention.

XX Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 21; Length 353;

Best Local Similarity 99.7%; Pred. No. 3.1e-196;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNECHYDKHMDFFYRNSNTDVTGKLVYLCVGFECLEFFFSNSLYTAAVIKNNK 60
DB 1 MNECHYDKHMDFFYRNSNTDVTGKLVYLCVGFECLEFFFSNSLYTAAVIKNNK 60
QY 61 FHEPPYYLLANLAADFFAGIAYVFLMNTGVSKTLYNRMFLRQGLDSSLTASTNL 120
DB 61 FHEPPYYLLANLAADFFAGIAYVFLMNTGVSKTLYNRMFLRQGLDSSLTASTNL 120
QY 121 LVIAVERHMSIMRMVHNSLTKKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSIA 180
DB 121 LVIAVERHMSIMRMVHNSLTKKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSIA 180
QY 181 PIYSRSYLVFWTWSNLMFLIMVYVLRIVYVKKRTNVLSPHTSGSISRRRTPKMLKT 240
DB 181 PIYSRSYLVFWTWSNLMFLIMVYVLRIVYVKKRTNVLSPHTSGSISRRRTPKMLKT 240
QY 241 VMTVLGAFVVCWTPGLVYVPLDGLNCRQCGVOHVAKRMFLLLALLNSVNPPIYSKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVYVPLDGLNCRQCGVOHVAKRMFLLLALLNSVNPPIYSKDEDM 300
QY 301 YGTMMKMICCFQSENPERRRPSRIPTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMMKMICCFQSENPERRRPSRIPTVLSRSDTGSQYIEDSISOGAVCNKSTS 353

RESULT 4

AAVS1227
ID AAVS1227 standard; Protein; 353 AA.

XX AAVS1227;

XX 06-APR-2000 (first entry)

XX Human G protein-coupled receptor protein.

XX

KM G protein-coupled receptor; human; lysophosphatidic acid; diagnosis;
KM treatment; prostate cancer; prostatic hyperplasia; inflammation.

XX Homo sapiens.

XX WO9967383-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-JP03306.

XX 22-JUN-1998; 98JP-0174731.

XX (NISB) JAPAN TOBACCO INC.

XX Nozaki Y, Naito T;

XX WPI; 2000-106293/09.

XX N-PSDB; AA244359.

XX G-protein coupled receptor protein binding to lysophosphatidic acid
XX used for treatment of prostate cancer -

XX Claim 1; Page 55-57; 67pp; Japanese.

CC This invention describes a novel human G-protein coupled receptor.
CC protein capable of binding lysophosphatidic acid, and proteins derived
CC from it by addition, deletion and/or substitution of one or more amino
CC acid residues. Antibodies to the protein are used for diagnosis of, and
CC agonists/antagonists to the protein are used for the treatment of,
CC prostatic disorders such as prostate cancer, benign prostatic
CC hyperplasia, and inflammation of the prostate. This sequence represents
CC the human G protein-coupled receptor protein described in the method of
CC the invention.

XX Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 21; Length 353;

Best Local Similarity 99.7%; Pred. No. 3.1e-196;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNECHYDKHMDFFYRNSNTDVTGKLVYLCVGFECLEFFFSNSLYTAAVIKNNK 60
DB 1 MNECHYDKHMDFFYRNSNTDVTGKLVYLCVGFECLEFFFSNSLYTAAVIKNNK 60
QY 61 FHEPPYYLLANLAADFFAGIAYVFLMNTGVSKTLYNRMFLRQGLDSSLTASTNL 120
DB 61 FHEPPYYLLANLAADFFAGIAYVFLMNTGVSKTLYNRMFLRQGLDSSLTASTNL 120
QY 121 LVIAVERHMSIMRMVHNSLTKKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSIA 180
DB 121 LVIAVERHMSIMRMVHNSLTKKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSIA 180
QY 181 PIYSRSYLVFWTWSNLMFLIMVYVLRIVYVKKRTNVLSPHTSGSISRRRTPKMLKT 240
DB 181 PIYSRSYLVFWTWSNLMFLIMVYVLRIVYVKKRTNVLSPHTSGSISRRRTPKMLKT 240
QY 241 VMTVLGAFVVCWTPGLVYVPLDGLNCRQCGVOHVAKRMFLLLALLNSVNPPIYSKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVYVPLDGLNCRQCGVOHVAKRMFLLLALLNSVNPPIYSKDEDM 300
QY 301 YGTMMKMICCFQSENPERRRPSRIPTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMMKMICCFQSENPERRRPSRIPTVLSRSDTGSQYIEDSISOGAVCNKSTS 353

RESULT 5

AAE04563
ID AAE04563 standard; Protein; 353 AA.

XX AAE04563;

XX 04-SEP-2001 (first entry)

XX

Human G-protein coupled receptor-19 (GRCRC-19) protein.

Human G-protein coupled receptor-19; GRCRC-19; gene therapy; cirrhosis; transgenic animal; proliferative disorder; actinic keratosis; hepatitis; nephrotropic; cancer; breast; bladder; bone marrow; brain; uterus; leukaemia; adenocarcinoma; lymphoma; melanoma; myeloma; epilepsy; stroke; Huntington's disease; multiple sclerosis; dementia; angina pectoris; central nervous system disorder; cardiovascular disorder; hypertension; atherosclerosis; congestive heart failure; gastrointestinal disorder; dysphagia; peptic oesophagitis; spasm; gastritis; anorexia; pyrosis; pancreatitis; Crohn's disease; diarrhoea; autoimmune disorder; anaemia; inflammatory disorder; Acquired Immune Deficiency Syndrome; AIDS; Addison's diseases; allergy; asthma; diabetes mellitus; antithyroid; atopic dermatitis; glomerulonephritis; Grave's disease; psoriasis; rheumatoid arthritis; ulcerative colitis; osteoporosis; antifungal; metabolic disorder; obesity; nontropic; protozoacide; virucide.

Homo sapiens.

Key Location/Qualifiers

Domain 36..56 /label= Transmembrane_domain

Domain 146..166 /label= Transmembrane_domain

Domain 187..207 /label= Transmembrane_domain

Domain 240..258 /label= Transmembrane_domain

MO200142288-A2.

14-JUN-2001.

07-DEC-2000; 2000MO-US33382.

10-DEC-1999; 9905-0172852.

22-DEC-1999; 9905-0171732.

14-JAN-2000; 2000US-0176148.

21-JAN-2000; 2000US-0177331.

(INCY-) INCYTE GENOMICS INC.

Burford N, Baughn MR, Au-Young J, Yang J, Lu DM, Reddy R;

WPI; 2001-381635/40.

N-PSDB; AAD08853.

New human G-protein coupled receptor polypeptides for diagnosing,

preventing, and treating cell proliferative, neurological,

cardiovascular, gastrointestinal, autoimmune and metabolic disorders

Claim 1; Page 142; 175pp; English.

The present sequence is human G-protein coupled receptor-19 (GRCRC-19) protein. GRCRC is useful in somatic or germ-line gene therapy to correct a genetic deficiency, to express a conditionally lethal gene product and to express a protein which affords protection against intracellular parasites and also for diagnosis of disorders associated with expression of GRCRC. GRCRC is also useful for generating hybridisation probes useful in mapping the naturally occurring genomic sequences and to create knock-in humanised animals (pigs) or transgenic animals (mice or rats) to model human diseases. GRCRC is used to diagnose, prevent and treat proliferative disorders (actinic keratosis, arteriosclerosis, cirrhosis, hepatitis and cancer); cancer (breast, bladder, bone marrow, brain, uterus cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma) neurological disorders (epilepsy, stroke, Alzheimer's, Huntington's, Parkinson's disease, multiple sclerosis, dementia and other central nervous system disorders); cardiovascular disorders (angina pectoris, hypertension, atherosclerosis, congestive heart failure); gastrointestinal disorders (dysphagia, peptic oesophagitis, oesophageal spasm, gastritis, gastric carcinoma, anorexia, nausea, abdominal angina,

pyrosis, pancreatitis, Crohn's disease, diarrhoea); autoimmune/inflammatory disorders (acquired immunodeficiency syndrome (AIDS), Addison's diseases, allergies, anaemia, asthma, diabetes mellitus, atopic dermatitis, glomerulonephritis, Grave's disease, osteoarthritis, fungal, psoriasis, rheumatoid arthritis, ulcerative colitis, bacterial, fungal, parasitic, protozoal and helminthic infections) and metabolic disorders (obesity, osteoporosis, viral infections).

Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 22; Length 353;

Best Local Similarity 99.7%; Pred. No. 3.1e-156;

Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MNECHYKHMDFNRSNTDVTDMGKLYIVCAGFCLFFFSNSLYIAVIRNK 60

1 MNECHYKHMDFNRSNTDVTDMGKLYIVCAGFCLFFFSNSLYIAVIRNK 60

61 FHEPFYLLANLAADFPAGIAYVFLMFTGTPSVSKITLVNRMFLROGLDSSLTASLTNT 120

61 FHEPFYLLANLAADFPAGIAYVFLMFTGTPSVSKITLVNRMFLROGLDSSLTASLTNT 120

121 LVIAVERHMSIMRRVNSNLTFRKVTLLILVMAIAIFPKGAVPTLGNKCLNISACSSLA 180

121 LVIAVERHMSIMRRVNSNLTFRKVTLLILVMAIAIFPKGAVPTLGNKCLNISACSSLA 180

181 PIYSRSYLVFWTNSNLAFLIMVVYRIYVYVYRKNTVLSPTSGSISRRRPMKMKT 240

181 PIYSRSYLVFWTNSNLAFLIMVVYRIYVYVYRKNTVLSPTSGSISRRRPMKMKT 240

241 VMTVLGAFVVCWTPGLVLPDLGLNCRQCGVQVHKRMFLLLALLNSVYVNPILYSKXEDM 300

241 VMTVLGAFVVCWTPGLVLPDLGLNCRQCGVQVHKRMFLLLALLNSVYVNPILYSKXEDM 300

301 YGTMKMKICGSOENPERPSRIPSTVLSRSDSGSYIEDISGAVCNKSTS 353

301 YGTMKMKICGSOENPERPSRIPSTVLSRSDSGSYIEDISGAVCNKSTS 353

Db

RESULT 6

ABG96440 standard; Protein: 353 AA.

ABG96440;

11-DEC-2002 (first entry)

Human ovarian cancer marker OV77.

Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasia; histological type; carcinogenic; ovarian cancer marker.

Homo sapiens.

MO200271928-A2.

19-SEP-2002.

14-MAR-2002; 2002MO-US07826.

14-MAR-2001; 2001US-276025P.

10-AUG-2001; 2001US-276026P.

10-AUG-2001; 2001US-311732P.

19-SEP-2001; 2001US-323580P.

26-SEP-2001; 2001US-324967P.

26-SEP-2001; 2001US-325102P.

26-SEP-2001; 2001US-325149P.

(MILL-) MILLENNIUM PHARM INC.

PA Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
PI Meyers RE, Morrisey MP, Olandt PJ, Sen A, Vlehey PO, Mills GB;
PI Baet RC, Lu K, Schmandt RE, Zhao X, Glatk K;
XX WPI: 2002-723277/78.
XX N-PSDB: AB575539.

Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient -

Disclosure: Page 457-458; 481pp; English.

The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterizing cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. non-tuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present amino acid sequence represents one of the ovarian cancer markers described in the invention.

Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 23; Length 353;

Best Local Similarity 99.7%; Pred. No. 3,1e-196;

Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 MNECHYDKHMDFFNRSNTDVTVDWGTGKLYIVLCVGTFFCLFFFSNSLYIAAVIKNRK 60
1 MNECHYDKHMDFFNRSNTDVTVDWGTGKLYIVLCVGTFFCLFFFSNSLYIAAVIKNRK 60
DB 61 FHFFPYLLANLAADFPAGTAYVFLMFNTPVSKTLLVNMFLROGLDSSLASLNL 120
61 FHFFPYLLANLAADFPAGTAYVFLMFNTPVSKTLLVNMFLROGLDSSLASLNL 120
DB 61 FHFFPYLLANLAADFPAGTAYVFLMFNTPVSKTLLVNMFLROGLDSSLASLNL 120
61 FHFFPYLLANLAADFPAGTAYVFLMFNTPVSKTLLVNMFLROGLDSSLASLNL 120
DB 121 LVIAVERHMSIMRNRVSNLTKKRVTLILVMAIAFMGAVPTLGMNCLNISACSSIA 180
121 LVIAVERHMSIMRNRVSNLTKKRVTLILVMAIAFMGAVPTLGMNCLNISACSSIA 180
DB 121 LVIAVERHMSIMRNRVSNLTKKRVTLILVMAIAFMGAVPTLGMNCLNISACSSIA 180
121 LVIAVERHMSIMRNRVSNLTKKRVTLILVMAIAFMGAVPTLGMNCLNISACSSIA 180
DB 181 PIYRSRLVPTVSNLAFLIMVYVLRITYYVKKRKNVLSPHSGISRRRTPKMLKT 240
181 PIYRSRLVPTVSNLAFLIMVYVLRITYYVKKRKNVLSPHSGISRRRTPKMLKT 240
DB 181 PIYRSRLVPTVSNLAFLIMVYVLRITYYVKKRKNVLSPHSGISRRRTPKMLKT 240
181 PIYRSRLVPTVSNLAFLIMVYVLRITYYVKKRKNVLSPHSGISRRRTPKMLKT 240
DB 241 VMTVLGAFVVCWTGVLVLLDGLNRCQGVQVHKRWFLLALINSVNPPIYYSKDDDM 300
241 VMTVLGAFVVCWTGVLVLLDGLNRCQGVQVHKRWFLLALINSVNPPIYYSKDDDM 300
DB 241 VMTVLGAFVVCWTGVLVLLDGLNRCQGVQVHKRWFLLALINSVNPPIYYSKDDDM 300
241 VMTVLGAFVVCWTGVLVLLDGLNRCQGVQVHKRWFLLALINSVNPPIYYSKDDDM 300
DB 301 YGTNKKMICFSQENPERRPSRIPSTVLSRSDTGSQYIEDSIQAGAVCNKSTS 353
301 YGTNKKMICFSQENPERRPSRIPSTVLSRSDTGSQYIEDSIQAGAVCNKSTS 353

RESULT 7

ABG61898
ID ABG61898 standard; Protein; 353 AA.

XX AC ABG61898;

DB 15-AUG-2002 (first entry)

DE Prostate cancer-associated protein #99.

KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.

XX Mammalia.

PN WO200230268-A2.

PD 18-APR-2002.

PF 12-OCT-2001; 2001WO-US32045.

PR 13-OCT-2000; 2000US-0687576.

PR 08-DEC-2000; 2000US-0733288.

PR 08-DEC-2000; 2000US-0733742.

PR 24-JAN-2001; 2001US-263857P.

PR 16-MAR-2001; 2001US-276791P.

PR 16-MAR-2001; 2001US-276888P.

PR 06-APR-2001; 2001US-281922P.

PR 24-APR-2001; 2001US-286214P.

PR 30-APR-2001; 2001US-0847045.

PR 04-MAY-2001; 2001US-286889P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

PS Claim 27; Page 385; 436pp; English.

CC The present invention relates to methods of detecting a prostate

CC cancer-associated transcript in a cell from a patient. The method

CC comprises contacting a biological sample from the patient with

CC prostate cancer-associated polynucleotides (designated PC genes) that

CC selectively hybridize to a sequence that is at least 80% identical

CC to them. The prostate cancer-associated polynucleotide sequences

CC are differentially expressed in prostate tumour tissue or in

CC prostate cancer and are derived from the tissues of various

CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).

CC The methods of the invention are useful for diagnosing and treating

CC prostate cancer in mammals. The prostate cancer-associated genes are

CC useful for diagnosing or treating prostate cancer, as well as for

CC identifying modulators of prostate cancer or agents that inhibit

CC prostate cancer. The nucleic acid sequences are particularly useful

CC in gene therapy, as a vaccine or in antisense applications.

CC ABG61800-ABG61944 represent prostate cancer-associated proteins.

XX Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 23; Length 353;

Best Local Similarity 99.7%; Pred. No. 3,1e-196;

Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 MNECHYDKHMDFFNRSNTDVTVDWGTGKLYIVLCVGTFFCLFFFSNSLYIAAVIKNRK 60
1 MNECHYDKHMDFFNRSNTDVTVDWGTGKLYIVLCVGTFFCLFFFSNSLYIAAVIKNRK 60

QY 61 FHEPEYLLANLAADFFACIAVFLMFNTGPNVSKTLTVNRKFLRQGLDSSLTASTLNL 120
 CC |||||||
 CC 61 FHEPEYLLANLAADFFACIAVFLMFNTGPNVSKTLTVNRKFLRQGLDSSLTASTLNL 120
 Db |||||||
 QY 121 LVIAVERHMSIMRRVHNSNLTKKRVTLILLVAIAIFMGAVPLGNNCLNTSACSLSA 180
 CC |||||||
 CC 121 LVIAVERHMSIMRRVHNSNLTKKRVTLILLVAIAIFMGAVPLGNNCLNTSACSLSA 180
 Db |||||||
 QY 181 PYSRSYLVEWTVSNLMAFLIMVYVLRIVYVKRKTNLSPHTSGSISRRTPMKLMKT 240
 CC |||||||
 CC 181 PYSRSYLVEWTVSNLMAFLIMVYVLRIVYVKRKTNLSPHTSGSISRRTPMKLMKT 240
 Db |||||||
 QY 241 VMTVLGAFVVCWTPGLVLPDLGNCRCQGVQHKRFFLLALLNSVYVNPITISYKDEDM 300
 CC |||||||
 CC 241 VMTVLGAFVVCWTPGLVLPDLGNCRCQGVQHKRFFLLALLNSVYVNPITISYKDEDM 300
 Db |||||||
 QY 301 YGTMKMKICFSEQENPERRPSRIPSTVLSRSDGSOYIEDSISOGAVCNKSTS 353
 CC |||||||
 CC 301 YGTMKMKICFSEQENPERRPSRIPSTVLSRSDGSOYIEDSISOGAVCNKSTS 353
 Db |||||||

SOLIT 8

ABR48221
 ID ABR48221 standard; protein; 353 AA.

AC ABR48221:
 XX
 DT 12-JUN-2003 (first entry)
 XX

DE Human bladder cancer associated protein sequence SEQ ID NO:162.

KM Human: bladder cancer; cytostatic; gene therapy; vaccine.

OS Homo sapiens.

XX WO2003003906-A2.

XX 16-JAN-2003.

PF 03-JUL-2002; 2002WO-US21338.

XX 03-JUL-2001; 2001US-302814P.

PR 03-AUG-2001; 2001US-310099P.

PR 08-NOV-2001; 2001US-343705P.

PR 13-NOV-2001; 2001US-350666P.

PR 12-APR-2002; 2002US-372246P.

XX (ECSB-) EOS BIOTECHNOLOGY INC.

PA Mack DH, Aziz N;

DR WPI; 2003-201532/19.

XX N-PSDB; ACC51036.

XX

PS

XX

CC

CC

CC

CC

CC

CC

Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody

Claim 10; Page 285-286; 307pp; English.

The present invention describes a method for detecting a bladder cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 encode the human bladder cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in

CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications.
 CC
 XX

SO Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 24; Length 353;
 Best Local Similarity 99.7%; Pred. No. 3.1e-196;
 Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNECHYKHMDFYNSRNTDPTVDMGTGKVIYLCVGFCLTFPSNSLVIAVKNRK 60
 Db |||||||
 Db 1 MNECHYKHMDFYNSRNTDPTVDMGTGKVIYLCVGFCLTFPSNSLVIAVKNRK 60
 QY 61 FHEPEYLLANLAADFFACIAVFLMFNTGPNVSKTLTVNRKFLRQGLDSSLTASTLNL 120
 CC |||||||
 CC 61 FHEPEYLLANLAADFFACIAVFLMFNTGPNVSKTLTVNRKFLRQGLDSSLTASTLNL 120
 Db |||||||
 QY 121 LVIAVERHMSIMRRVHNSNLTKKRVTLILLVAIAIFMGAVPLGNNCLNTSACSLSA 180
 CC |||||||
 CC 121 LVIAVERHMSIMRRVHNSNLTKKRVTLILLVAIAIFMGAVPLGNNCLNTSACSLSA 180
 Db |||||||
 QY 181 PYSRSYLVEWTVSNLMAFLIMVYVLRIVYVKRKTNLSPHTSGSISRRTPMKLMKT 240
 CC |||||||
 CC 181 PYSRSYLVEWTVSNLMAFLIMVYVLRIVYVKRKTNLSPHTSGSISRRTPMKLMKT 240
 Db |||||||
 QY 241 VMTVLGAFVVCWTPGLVLPDLGNCRCQGVQHKRFFLLALLNSVYVNPITISYKDEDM 300
 CC |||||||
 CC 241 VMTVLGAFVVCWTPGLVLPDLGNCRCQGVQHKRFFLLALLNSVYVNPITISYKDEDM 300
 Db |||||||
 QY 301 YGTMKMKICFSEQENPERRPSRIPSTVLSRSDGSOYIEDSISOGAVCNKSTS 353
 CC |||||||
 CC 301 YGTMKMKICFSEQENPERRPSRIPSTVLSRSDGSOYIEDSISOGAVCNKSTS 353
 Db |||||||

RESULT 9

ABP59287
 ID ABP59287 standard; protein; 353 AA.

XX ABP59287;

DT 10-MAY-2003 (first entry)

XX Human Edg7 receptor.

DE Human; Edg; receptor.

KM Human; Edg; receptor.

XX Homo sapiens.

XX WO2003006503-A1.

XX 23-JAN-2003.

PF 10-JUL-2002; 2002WO-US22346.

XX 11-JUL-2001; 2001US-0904099.

XX (CERE-) CERRETER.

PA Shanker G, Munning JN, Spencer JV;

DR WPI; 2003-221718/21.

XX

XX

XX

XX

XX

The present invention relates to Edg receptors (ABP59277-ABP59290). The Edg receptors, are useful in a high-throughput screening assay to identify compounds that bind to or modulate the activity of the polypeptide, in calcium mobilisation assays, binding assays, detection of

CC CAMP formation, or in reporter gene techniques.

XX Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 24; Length 353;

Best Local Similarity 99.7%; Pred. No. 3.1e-196; Mismatches 1; Indels 0; Gaps 0;

Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MNECHYDKHMDFFNRSNTDVTVDWGTGKLYIVLCVGTFFCLIFPFSNSLYIAAVIKNRK 60
DB 1 MNECHYDKHMDFFNRSNTDVTVDWGTGKLYIVLCVGTFFCLIFPFSNSLYIAAVIKNRK 60
QY 61 FHFPFYLLANLAADFFAGIAVYFLMNTGCVSTLYVNRKFLRQGLDSSLTASLTNL 120
DB 61 FHFPFYLLANLAADFFAGIAVYFLMNTGCVSTLYVNRKFLRQGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMRMVHNSLTKRRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180
DB 121 LVIAVERHMSIMRMVHNSLTKRRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180
QY 181 PIYSRSYLVFWTVSNLMAFLIMVYVYLRIVYVKKRTNVLSPHTSGSISRRTPKLTKMT 240
DB 181 PIYSRSYLVFWTVSNLMAFLIMVYVYLRIVYVKKRTNVLSPHTSGSISRRTPKLTKMT 240
QY 241 VMTVLGAFVVCWTPGLVYLLPDGLNCRGCGVQVHKRMFLALLALNSVNPPIIYSKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVYLLPDGLNCRGCGVQVHKRMFLALLALNSVNPPIIYSKDEDM 300
QY 301 YGTMKMKICFSGOENPERPRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKMKICFSGOENPERPRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
```

RESULT 10
ABU56733
ID ABU56733 standard; Protein; 353 AA.

XX AC ABU56733;

XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polypeptide #326.

XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;

XX KW antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;

XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX OS Unidentified.

XX PN WO200286443-A2.

XX PD 31-OCT-2002.

XX PF 18-APR-2002; 2002WO-US12476.

XX PR 18-APR-2001; 2001US-284770P.

XX PR 10-MAY-2001; 2001US-290492P.

XX PR 09-NOV-2001; 2001US-339245P.

XX PR 13-NOV-2001; 2001US-350666P.

XX PR 29-NOV-2001; 2001US-334370P.

XX PR 12-APR-2002; 2002US-372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Aziz N, Murray R;

XX DR WPI; 2003-093161/08.

XX DR N-PSDB; ABX76462.

XX PT Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the

PT patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer -

PS Claim 27; Page 440; 453pp; English.

CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC method are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated
CC polypeptides of the invention.

XX SQ Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 24; Length 353;

Best Local Similarity 99.7%; Pred. No. 3.1e-196; Mismatches 1; Indels 0; Gaps 0;

Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MNECHYDKHMDFFNRSNTDVTVDWGTGKLYIVLCVGTFFCLIFPFSNSLYIAAVIKNRK 60
DB 1 MNECHYDKHMDFFNRSNTDVTVDWGTGKLYIVLCVGTFFCLIFPFSNSLYIAAVIKNRK 60
QY 61 FHFPFYLLANLAADFFAGIAVYFLMNTGCVSTLYVNRKFLRQGLDSSLTASLTNL 120
DB 61 FHFPFYLLANLAADFFAGIAVYFLMNTGCVSTLYVNRKFLRQGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMRMVHNSLTKRRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180
DB 121 LVIAVERHMSIMRMVHNSLTKRRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180
QY 181 PIYSRSYLVFWTVSNLMAFLIMVYVYLRIVYVKKRTNVLSPHTSGSISRRTPKLTKMT 240
DB 181 PIYSRSYLVFWTVSNLMAFLIMVYVYLRIVYVKKRTNVLSPHTSGSISRRTPKLTKMT 240
QY 241 VMTVLGAFVVCWTPGLVYLLPDGLNCRGCGVQVHKRMFLALLALNSVNPPIIYSKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVYLLPDGLNCRGCGVQVHKRMFLALLALNSVNPPIIYSKDEDM 300
QY 301 YGTMKMKICFSGOENPERPRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKMKICFSGOENPERPRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
```

RESULT 11
ABP81689
ID ABP81689 standard; Protein; 353 AA.

XX AC ABP81689;

XX DT 04-MAR-2003 (first entry)

XX DE Human lysophosphatidic acid receptor Edg7 protein SEQ ID NO:553.

XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

XX KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

XX KW immunological-related disease; cell proliferative disease; autoimmune disease;

XX KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

XX KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

XX KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 KW Homo sapiens.
 XX MO200261087-A2.
 PN 08-AUG-2002.
 PD 19-DEC-2001; 2001WO-US50107.
 PF 19-DEC-2000; 2000US-257144P.
 PR (LIFE-) LIFESPAN BIOSCIENCES INC.
 PA Burner GC, Roush CL, Brown JP;
 XX
 XX WPI: 2003-046718/04.
 DR N-PSDB; ABZ42535.
 XX
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases
 XX
 PS Disclosure; Fig 1; 523pp; English.
 XX
 CC The present invention describes antigenic peptides (1) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.
 CC
 XX
 SO Sequence 353 AA;
 QY Query Match 99.5%; Score 1838; DB 24; Length 353;
 Db Best Local Similarity 99.7%; Pred. No. 3.1e-196;
 Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNECHYKHMDEFNRSNTDVTVDWGTGKLYIVLCVGTFFCLFFFSNSLYIAVINRK 60
 Db 1 MNECHYKHMDEFNRSNTDVTVDWGTGKLYIVLCVGTFFCLFFFSNSLYIAVINRK 60
 QY 61 FHPFFYLLANTLAADFFAGIAYVFLMNTGPKYKTLVNRWFLRQGLDSSLTASLTNL 120
 Db 61 FHPFFYLLANTLAADFFAGIAYVFLMNTGPKYKTLVNRWFLRQGLDSSLTASLTNL 120
 QY 121 LVIAVERHMSIMRKRVSNTLTKRKRVTLILLVMAIAIFMGAVPTLGNCLCNISACSSLA 180
 Db 121 LVIAVERHMSIMRKRVSNTLTKRKRVTLILLVMAIAIFMGAVPTLGNCLCNISACSSLA 180

QY 181 PIYRSILVETVSNLMAFLIMVYVYLRITYYRKRNINVSPTHTSGISRRTPMKLMKT 240
 Db 181 PIYRSILVETVSNLMAFLIMVYVYLRITYYRKRNINVSPTHTSGISRRTPMKLMKT 240
 QY 241 VMTVLGAFVVCWTFGLVLLPLDGLNCRQCGVQHKRNFLLALNSVNPPIYSKQEDM 300
 Db 241 VMTVLGAFVVCWTFGLVLLPLDGLNCRQCGVQHKRNFLLALNSVNPPIYSKQEDM 300
 QY 301 YGTMKMICFSDENPERPSPRIPSTVLSRSDTGSQYIEDSISGAVCNKSTKS 353
 Db 301 YGTMKMICFSDENPERPSPRIPSTVLSRSDTGSQYIEDSISGAVCNKSTKS 353
 RESULT 12
 AAY24242
 ID AAY24242 standard; Protein; 353 AA.
 XX
 AC AAY24242;
 XX
 DT 13-SEP-1999 (first entry)
 DT
 DE Human EDG-5 receptor clone pc3-hedg5#28 protein.
 KW EDG-5; HEDG-5; receptor homologue; asthma; rheumatoid arthritis;
 KW adult respiratory distress syndrome; cardiac ischemia; septic shock;
 KW acute pancreatitis; psoriasis; acute cyclosporine nephrotoxicity;
 KW early diabetic glomerulopathy; lung damage.
 XX
 OS Homo sapiens.
 OS
 XX W09933972-A1.
 XX
 PD 08-JUL-1999.
 XX
 PF 24-DEC-1998; 98WO-CA01193.
 XX
 PR 24-DEC-1997; 97US-0997803.
 XX
 PA (ALIX) ALLELIX BIOPHARMACEUTICALS INC.
 XX
 PI Chun JYM, Gupta AK, Munroe DG, Vyas TB;
 DR WPI: 1999-419106/35.
 DR N-PSDB; MAX86747.
 XX
 CC Nucleotide sequences encoding mammalian EDG-5 receptors
 CC
 PS Claim 13; Fig 4C; 87pp; English.
 CC
 CC The present sequence is a human EDG-5 (HEDG-5) receptor homologue.
 CC EDG-5 sequences may be used to test for aberrant expression of HEDG-5
 CC and can accelerate diagnosis and proper treatment of conditions such as
 CC adult respiratory distress syndrome, asthma, rheumatoid arthritis,
 CC cardiac ischemia, acute pancreatitis, septic shock, psoriasis, acute
 CC cyclosporine nephrotoxicity and early diabetic glomerulopathy, as well
 CC as lung damage following exposure to cigarette smoke, asbestos, or
 CC silica. HEDG-5 specific antibodies, inhibitors and ligands may be used
 CC to treat inflammation or diseases including, viral, bacterial or fungal
 CC infections, allergic responses, mechanical injury associated with
 CC trauma, hereditary diseases, lymphoma or carcinoma, or other conditions
 CC which activate the genes of kidney, lung, heart, lymphoid or tissues of
 CC the nervous system.
 CC
 XX
 SO Sequence 353 AA;
 QY Query Match 99.2%; Score 1834; DB 20; Length 353;
 Db Best Local Similarity 99.4%; Pred. No. 8.5e-196;
 Matches 351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MNECHYKHMDEFNRSNTDVTVDWGTGKLYIVLCVGTFFCLFFFSNSLYIAVINRK 60
 Db 1 MNECHYKHMDEFNRSNTDVTVDWGTGKLYIVLCVGTFFCLFFFSNSLYIAVINRK 60

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QY 61 FHFPEYLLANLAADFPAGIAYVFLMNTGVSKTLLVNRWFLRQGLDSSLTASLTNL 120
DB 61 FHFPEYLLANLAADFPAGIAYVFLMNTGVSKTLLVNRWFLRQGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMRMRVHNSLTKRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSLA 180
DB 121 LVIAVERHMSIMRMRVHNSLTKRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSLA 180
QY 181 PIYSRSYLVFMTVSNLMAFLIMVYVYLRIVYVKKRTNVLSPHTSGSISRRTTPMKLMKT 240
DB 181 PIYSRSYLVFMTVSNLMAFLIMVYVYLRIVYVKKRTNVLSPHTSGSISRRTTPMKLMKT 240
QY 241 VMTVLGAFVVCWTPGLVYLLPLDGLNCRCCGVQVHVRKRWFLALLNSVNPPIIYSYKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVYLLPLDGLNCRCCGVQVHVRKRWFLALLNSVNPPIIYSYKDEDM 300
QY 301 YGTMMKMICFSQENKERRPRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMMKMICFSQENKERRPRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353

```

RESULT 13

ABP56225
ID ABP56225 standard; Protein: 353 AA.

XX ABP56225;
AC
DT 28-MAR-2003 (first entry)

DE Human EDG7 receptor protein sequence.

KW Rat; EDG7 receptor; receptor; cytosolic; cancer.

OS Homo sapiens.

XX Key Location/Qualifiers

```

FT MISC-difference 57 /note= "unclear in specification"
FT MISC-difference 103 /note= "unclear in specification"
FT MISC-difference 118 /note= "unclear in specification"
FT MISC-difference 207 /note= "unclear in specification"
FT MISC-difference 305 /note= "unclear in specification"
FT MISC-difference 316 /note= "unclear in specification"
FT MISC-difference 338 /note= "unclear in specification"

```

XX JP2002238578-A.

PD 27-AUG-2002.

PF 20-FEB-2001; 2001JP-0043004.

PR 20-FEB-2001; 2001JP-0043004.

PA (NNSH) NIPPON SHINYAKU CO LTD.

DR WPI; 2003-049457/05.

XX Rat EDG7 receptor protein, useful for diagnosing and treating cancers

XX Example 2; Fig 1; 19pp; Japanese.

XX The present invention describes rat EDG7 receptor protein (I). Also
CC described: (1) a polynucleotide (II) encoding (I); (2) an oligonucleotide
CC which can hybridise with (II) under a stringent conditions; and
CC (3) a recombinant vector containing (II). (I) has cytosolic activity.
CC (I) can be used for diagnosing and treating cancers. The present sequence
CC represents a human EDG7 receptor protein, which is given in comparison

CC with the rat EDG7 receptor protein in an example from the present
CC invention.

XX Sequence 353 AA;

Query Match 96.0%; Score 1775; DB 24; Length 353;
Best Local Similarity 96.9%; Pred. No. 3,3e-189;
Matches 342; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```

QY 1 MNECHYDHMDPEYRSNTDQVDDMTGTRLVYVLCVGFECLEFFESNLVAAVYKRRK 60
DB 1 MNECHYDHMDPEYRSNTDQVDDMTGTRLVYVLCVGFECLEFFESNLVAAVYKRRK 60
QY 61 FHFPEYLLANLAADFPAGIAYVFLMNTGVSKTLLVNRWFLRQGLDSSLTASLTNL 120
DB 61 FHFPEYLLANLAADFPAGIAYVFLMNTGVSKTLLVNRWFLRQGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMRMRVHNSLTKRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSLA 180
DB 121 LVIAVERHMSIMRMRVHNSLTKRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSLA 180
QY 181 PIYSRSYLVFMTVSNLMAFLIMVYVYLRIVYVKKRTNVLSPHTSGSISRRTTPMKLMKT 240
DB 181 PIYSRSYLVFMTVSNLMAFLIMVYVYLRIVYVKKRTNVLSPHTSGSISRRTTPMKLMKT 240
QY 241 VMTVLGAFVVCWTPGLVYLLPLDGLNCRCCGVQVHVRKRWFLALLNSVNPPIIYSYKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVYLLPLDGLNCRCCGVQVHVRKRWFLALLNSVNPPIIYSYKDEDM 300
QY 301 YGTMMKMICFSQENKERRPRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMMKMICFSQENKERRPRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353

```

RESULT 14

AAAB12399
ID AAAB12399 standard; Protein: 354 AA.

AC AAAB12399;

DT 13-NOV-2000 (first entry)

DE Human HOFNH30 protein.

KW HOFNH30; G-protein coupled receptor; 7TM receptor; vaccine;
KW cancer; inflammation; autoimmune disease; Crohn's disease;
KW allergy; asthma; rheumatoid arthritis; CMS inflammation;
KW cerebellar degeneration; Alzheimer's disease; Parkinson's disease;
KW multiple sclerosis; stroke; osteoporosis; cardiovascular; kidney;
KW liver; hypotension; hypertension; acquired immune deficiency syndrome;
KW AIDS; male pattern baldness; bacterial; fungal; protozoan;
KW viral infections.

OS Homo sapiens.

PN WO200035954-A1.

XX 22-JUN-2000.

PF 17-DEC-1999; 99WO-US30177.

PR 18-DEC-1998; 98US-0215072.

PR 04-JUN-1999; 99US-0325897.

PA (SMK) SMITHKLINE BEECHAM CORP.

PI Tsui P, Ellis CE, Sathe GM, Van Horn S, Ames RS, Foley JJ;

DR Fitzgerald LR, Sarau HM, Chambers JK;

PT WPI: 2000-431572/37.
N-PSDB: AAA63092.
New human G-protein coupled receptor, designated HOFNH30, useful for

treating infections, and disorders including cancers, diabetes, asthma, and Parkinson's disease.

Claim 2; Page 41-42; 44pp; English.

The present sequence is the novel human G-protein coupled receptor, HORNH30. The HORNH30 receptor may be expressed in human embryonic kidney 293 (HEK293) cells. This allows ligand binding assays to be carried out. The HORNH30 DNA and protein may be used for diagnosing or treating cancer, inflammation, autoimmune disease, Crohn's disease, allergy, asthma, rheumatoid arthritis, CNS inflammation, cerebellar degeneration, Alzheimer's disease, Parkinson's disease, multiple sclerosis, stroke, osteoporosis, cardiovascular disease, kidney disease, liver disease, hypotension, hypertension, acquired immune deficiency syndrome (AIDS), male pattern baldness, and bacterial, fungal, protozoan and viral infections.

Sequence 354 AA;

Query Match 95.9%; Score 1772.5; DB 21; Length 354;
Best Local Similarity 96.0%; Pred. No. 6.3e-189;
Matches 340; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 MNECHYKHMDEFYNSNTDVTDDMTGKLYIVLCVGFPCLETFEFSNSLVIAAVINRK 60
DB 1 MNECHYKHMDEFYNSNTDVTDDMTGKLYIVLCVGFPCLETFEFSNSLVIAAVINRK 60
QY 61 FHFPEYLLANLAADFFAGIAYVFLMNTGVPVSKTLTVNRWFLROGLDLSLTASLTNL 120
DB 61 FHFPEYLLANLAADFFAGIAYVFLMNTGVPVSKTLTVNRWFLROGLDLSLTASLTNL 120
QY 121 LVIAVERHMSIMRRVHSNLTKKRVTLILLVMAIAIFMGAVPTLGWNCICNISACSSLA 180
DB 121 LVIAVERHMSIMRRVHSNLTKKRVTLILLVMAIAIFMGAVPTLGWNCICNISACSSLA 180
QY 181 PIYSRSYLIVFWTVSNLMAFLIMVYVRIYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
DB 181 PIYSRSYLIVFWTVSNLMAFLIMVYVRIYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
QY 241 VMTVLGAFVVCWPTGVLVLLPLDGLNCRCQGVQVHKRFFLLALLNSVYVNPPIIYSKDEDM 300
DB 241 VMTVLGAFVVCWPTGVLVLLPLDGLNCRCQGVQVHKRFFLLALLNSVYVNPPIIYSKDEDM 300
QY 301 YGTMKKMICCFSE-NPERRRSPRIPTVLSRSDTGSQYIEDSISQGAVCNKSTS 353
DB 301 YGTMKKMICCFSE-NPERRRSPRIPTVLSRSDTGSQYIEDSISQGAVCNKSTS 353

RESULT 15
56224

ABP56224 standard; Protein; 354 AA.

ABP56224;

28-MAR-2003 (first entry)

Rat EDG7 receptor protein SEQ ID NO:1.

Rat; EDG7 receptor; receptor; cytosolic; cancer.

Rattus norvegicus.

JP2002238578-A.

27-AUG-2002.

20-FEB-2001; 2001JP-0043004.

20-FEB-2001; 2001JP-0043004.

(NNSH) NIPPON SHINYAKU CO LTD.

WPI; 2003-049457/05.

DR N-PSDB; ABZ21907.

PT Rat EDG7 receptor protein, useful for diagnosing and treating cancers

PS Claim 1; Page 12; 19pp; Japanese.

The present sequence represents rat EDG7 receptor protein (I). Also described: (1) a polynucleotide (II) encoding (I); (2) an oligonucleotide which can hybridise with (II) under a stringent conditions; and (3) a recombinant vector containing (II). (II) has cytosolic activity. (I) can be used for diagnosing and treating cancers.

Sequence 354 AA;

Query Match 91.9%; Score 1697.5; DB 24; Length 354;
Best Local Similarity 91.0%; Pred. No. 1.5e-180;
Matches 322; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

QY 1 MNECHYKHMDEFYNSNTDVTDDMTGKLYIVLCVGFPCLETFEFSNSLVIAAVINRK 60
DB 1 MNECHYKHMDEFYNSNTDVTDDMTGKLYIVLCVGFPCLETFEFSNSLVIAAVINRK 60
QY 61 FHFPEYLLANLAADFFAGIAYVFLMNTGVPVSKTLTVNRWFLROGLDLSLTASLTNL 120
DB 61 FHFPEYLLANLAADFFAGIAYVFLMNTGVPVSKTLTVNRWFLROGLDLSLTASLTNL 120
QY 121 LVIAVERHMSIMRRVHSNLTKKRVTLILLVMAIAIFMGAVPTLGWNCICNISACSSLA 180
DB 121 LVIAVERHMSIMRRVHSNLTKKRVTLILLVMAIAIFMGAVPTLGWNCICNISACSSLA 180
QY 181 PIYSRSYLIVFWTVSNLMAFLIMVYVRIYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
DB 181 PIYSRSYLIVFWTVSNLMAFLIMVYVRIYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
QY 241 VMTVLGAFVVCWPTGVLVLLPLDGLNCRCQGVQVHKRFFLLALLNSVYVNPPIIYSKDEDM 300
DB 241 VMTVLGAFVVCWPTGVLVLLPLDGLNCRCQGVQVHKRFFLLALLNSVYVNPPIIYSKDEDM 300
QY 301 YGTMKKMICCFSE-NPERRRSPRIPTVLSRSDTGSQYIEDSISQGAVCNKSTS 353
DB 301 YGTMKKMICCFSE-NPERRRSPRIPTVLSRSDTGSQYIEDSISQGAVCNKSTS 353

Search completed: August 18, 2003, 15:09:49
Job time : 85 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 15:04:54 ; Search time 42 Seconds
(without alignments)
808.275 Million cell updates/sec

Title: US-09-581-252-14

Perfect score: 1848

Sequence: 1 MNECHYDKHMDFFYNRSNTD.....GSQYIEDSISQAVCNKSTS 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Final number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES.

Result No.	Score	Query Match	Length	DB ID	Description
1	948.5	51.3	364	2	JC5293
2	541	29.3	383	2	J53870
3	540.5	29.2	362	2	JC7559
4	537	29.1	378	2	JC5245
5	533.5	28.9	381	2	A35300
6	499	27.0	352	2	JC1465
7	352	19.0	330	2	A55689
8	351	19.0	330	2	SA0454
9	347	18.8	473	2	A33117
10	341	18.5	472	2	S17595
11	327.5	17.7	362	2	I65990
12	326.5	17.7	363	2	S48697
13	326	17.6	325	2	JC5592
14	325	17.6	372	2	I49008
15	314	17.0	325	2	I46416
16	312	16.9	325	2	JC2193
17	310.5	16.8	332	2	A57055
18	306	16.6	325	2	JN0764
19	302.5	16.4	180	2	E48909
20	295	16.0	323	2	SA3850
21	294	15.9	390	2	JN0268
22	293	15.9	389	2	S68422
23	292	15.8	390	2	S58126
24	291	15.7	323	2	S36636
25	290.5	15.7	386	2	A42688
26	289.5	15.7	386	2	S54153
27	289.5	15.7	386	2	S18637
28	289	15.6	347	2	S70364
29	287.5	15.6	360	2	B46647

30	283	15.3	374	2	I77467	serotonin receptor
31	279.5	15.1	377	2	S68423	serotonin receptor
32	273.5	14.8	377	2	B30341	G protein-coupled
33	272	14.7	360	2	S36750	cannabinoid recept
34	272	14.7	377	2	A53279	serotonin receptor
35	270	14.6	515	2	A40491	serotonin receptor
36	267	14.4	501	2	JH0447	alpha-1A-adrenergic
37	267	14.4	572	2	I39369	alpha-1A-adrenergic
38	265	14.3	509	2	A47174	serotonin receptor
39	264	14.3	332	2	JC1229	adenosine receptor
40	261	14.1	517	2	A45121	alpha-1B adrenergic
41	260	14.1	314	2	S71420	melanocortin 1 rec
42	258	14.0	477	2	S71323	alpha-1A adrenergic
43	258	14.0	515	2	JC1525	alpha-1A adrenergic
44	257.5	13.9	560	2	A38731	alpha-1A adrenergic
45	256.5	13.9	366	2	S26048	serotonin receptor

ALIGNMENTS

RESULT 1

JC5293

Lysophosphatidic acid receptor - human

N:Alternate names: Edg2 protein

C:Species: Homo sapiens (man)

C>Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 10-Dec-1999

C:Accession: JC5293

R:An, S.: Dickens, M.A.; Bleu, T.; Hallmark, O.G.; Goetzl, E.J.

Biochem. Biophys. Res. Commun. 231, 619-622, 1997

A:Title: Molecular cloning of the human Edg2 protein and its identification as a func

A:Reference number: JC5293; MUID:9724397; PMID:9070858

A:Contents: lung

A:Accession: JC5293

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-364 <A>

A:Cross-references: GB:U08011; NID:91857424; PIDN:AMC51139.1; PID:91857425

C:Superfamily: G protein-coupled receptor edg-1

Query Match	51.3%	Score 948.5	DB 2	Length 364
Best Local Similarity	51.6%	Pred. No. 2.9e-74		
Matches 175	Conservative 76	Mismatches 75	Indels 13	Gaps 5
QY	1	MNE--CHYDKHMDFFYNRSNTDVTDDW--TGFTLVIVLCVGFPCLEFFFSNLTVAAYIK 57		
DB	19	MNEPQCFYNESIAFTYNSGKHLATEMTVSKLVNGL--GIVCFIMLANLNVVAIVY 76		
QY	58	NKKFHPFYLLANLAADDFAGIAYVFLMFTGVSRTLVNRFILROGLDLSLTASTL 117		
DB	77	NRRFHPFYLLANLAADDFAGIAYVFLMFTGVSRTLVNRFILROGLDLSLTASTL 136		
QY	118	TNLVIAVERHMSIRMRVHSLTKRYTLTLVMAIAIENGAVPTLGMCNLSACS 177		
DB	137	ANLAIATIERHITVFRMOLHFRMSNRVAVVIVVIMVAIVGAIPIGVAMNIDCIENCS 196		
QY	178	SLAPYSRYLYEVNVMFLINVVYLRVYVKKRTNLSHTSGSISRRTPKTL 237		
DB	197	NNAPLISDYLVFALELVTFVAVVVLTAHFGVROPTMSHSSGPRRRRTPMASL 256		
QY	238	MKTVMVLGAFVVCWTPGLVVLPLDGLNCRQGVQVHRVWFLALLALNSVNPPIITYSKD 297		
DB	257	LKTVMVLGAFVVCWTPGLVVLPLDGLNCRQGVQVHRVWFLALLALNSVNPPIITYSKD 315		
QY	298	EDMTGTRKMKICFSQENP-----ERRPSRIPSTVYS 329		
DB	316	KEMSATFROILCCORSENPPTGPTSSDRSASLMTIILA 354		

RESULT 2

J53870

Edg-1 orphan receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 24-Sep-1999
 C/Accession: J53870
 R/Lao, D.C.; Brode, C.S.; Gaskin, A.A.; Borden, J.M.; MacLennan, A.J.
 Gene 149, 331-336, 1994
 A/Title: Cloning of the rat edg-1 immediate-early gene: expression pattern suggests dive
 A/Reference number: J53870; MUID:95047498; PMID:7959012
 A/Accession: J53870
 A/Status: preliminary; translated from GR/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-383 <RES>
 A/Cross-references: EMBL:U10303; NID:9595396; PIDN:AAA83418.1; PID:9595397
 C/Superfamily: G protein-coupled receptor edg-1

Query Match 29.3%; Score 541; DB 2; Length 383;
 Best Local Similarity 34.2%; Pred. No. 4.3e-39;
 Matches 117; Conservative 77; Mismatches 128; Indels 20; Gaps 7;

27 GTKIVLCVGFECLEIFFSNSLVIAVINKRKHFFHYLLANLAADFAGIAYFL 86
 45 GIKLTAVFL-LICCLILENIFVLITWTKKFFHMYFIGNALSLDLGAVAYAN 102
 87 MENTGPVSKITLVNRWFLROGLDLSIFASIFNLIVAVRHMSIMRVRHSNLTTRKVT 146
 103 LLSGATTYKLTLPQWFLREGSMFVALSAYSLAIAIEHYITMLKMLHNGSSRSF 162
 147 LLLLVAAIFMGAIVPLIGMNCINISACSLAPIYSRSLVFWYSNLMALFLMVY 206
 163 LLISACWVISTLGLPLMGNCISSLSSTVPLVHKHILCTVYFTLLISTVLY 222
 207 LRIIVYVKTNTVSPHTSGISRRRT--PMKLMTWVTVGAIVVCTPGLVLPD-G 263
 223 CRISIVTRRRLTFKRNKISKASRSSEKSLALKTVIIVLSVLIACAPFIILLDVG 282
 264 LNCQGVQVHKRFFLLALINSVNPITISYKDEDMGTMKMICFSQENPE----R 318
 283 CKATCKTILYKAEFLVAVINSCTNPIIYLVTKMKRRAFIIRIISCKCPNGDSAGKFK 342
 319 RPSRIPSTVLSR--SDTGSQYIEDS-----ISGAVCNKS 351
 343 RPI-IPMERFSKSDNSHPQKDDGNDPETIMSSGNVSS 383

RESULT 3
 J53559
 sphingosine 1-phosphate receptor - zebra fish
 N/Alternate names: endothelial differentiation gene 1 receptor
 C/Species: Brachydanio rerio (zebra fish)
 C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
 Accession: J53559
 A/Map position: 100, D.S.; Ungar, A.R.; Lynch, K.R.
 Biochem. Biophys. Res. Commun. 279, 139-143, 2000
 A/Title: Characterization of a zebrafish (Danio rerio) sphingosine 1-phosphate receptor
 A/Reference number: J53559; MUID: 20363813; PMID:11112429
 A/Accession: J53559
 A/Molecule type: DNA
 A/Residues: 1-362 <IMA>
 A/Cross-references: GB:AF321294
 C/Comment: This receptor, a G protein-coupled receptor, mediates sphingosine 1-phosphate
 or also functions in the developing central nervous system in cell proliferation, apopto
 C/Genetics:
 A/Gene: edg1
 C/Superfamily: G protein-coupled receptor edg-1
 C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.2%; Score 540.5; DB 2; Length 362;
 Best Local Similarity 34.3%; Pred. No. 4.5e-39;
 Matches 113; Conservative 68; Mismatches 129; Indels 19; Gaps 5;

41 CLTFFNSLVIAVINKRKHFFHYLLANLAADFAGIAYFLMNTGPVSKITLVN 100
 35 CCEIIEVAVLITWTKKFFHMYFIGNALSLDLGAVAYANILSGANTYKLTPT 94
 101 RWFLROGLDLSIFASIFNLIVAVRHMSIMRVRHSNLTTRKVTLLLVAAIFMG 160

Db 95 QWFFREGSMFVALASVSLAIAIERHILMLKRLHNGKTCVFMILSTVWPIAIIIG 154
 161 AVPLIGMNCINISACSLAPIYSRSLVFWYSNLMALFLMVYVRIYVVRKTNVL 220
 155 GLPVMGNKCIDISNCSVPLVPLVHKATVIFCTVPSVILMAIVLVARIVALTFRSKL 214
 221 ----SPHTSGISRRRTPMKIMKTVMVVGAFVVCWPGVLVPLDGLNCR--OCGVQHV 274
 215 VERRVANGRGSKNSSEKSMALLKTVIIVLSQFIACMAPLFIILLD-VACQTFCSILYK 273
 275 KRWFLALINSVNPITISYKDEDMGTMKMICFSQENPE--RPSRIPSTVLSRS 331
 274 AEWFLALAVLSAMPILTYITLSNEMRAFTKMLNCGVQVSGKFSRPIWGAFFSTKS 333
 332 DTGSQYIEDS-----ISGAVCNKS 351
 334 DNSHPMKNDPEYSAPRETVSSGNITSSS 362

RESULT 4
 J5245
 G protein-coupled receptor - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 C/Accession: J5245
 R/Yamauchi, F.; Tokuda, M.; Hatake, O.; Brenner, S.
 Biochem. Biophys. Res. Commun. 227, 608-614, 1996
 A/Title: Molecular cloning of the novel human G protein-coupled receptor (GPCR) gene
 A/Reference number: J5245; MUID:97032811; PMID:8878560
 A/Accession: J5245
 A/Molecule type: DNA
 A/Residues: 1-378 <YAM>
 A/Cross-references: EMBL:X83864; NID:91770395; PIDN:CAA58744.1; PID:91770396
 C/Comment: This protein transduces hormone and neurotransmitter signals into intracel
 C/Genetics:
 A/Gene: edg-3
 A/Map position: 9q22.1-q22.2
 C/Superfamily: G protein-coupled receptor edg-1
 C/Keywords: G protein-coupled receptor

Query Match 29.1%; Score 537; DB 2; Length 378;
 Best Local Similarity 34.9%; Pred. No. 9.5e-39;
 Matches 122; Conservative 68; Mismatches 124; Indels 36; Gaps 9;

27 GTKIVLCVGFECLEIFFSNSLVIAVINKRKHFFHYLLANLAADFAGIAYFL 86
 38 GSTLTIVLFL-VICSPVLENIMVLAIVKRNKFFHMYFIGNALCIDLAGIAYVN 95
 87 MENTGPVSKITLVNRWFLROGLDLSIFASIFNLIVAVRHMSIMRVRHSNLTTRKVT 146
 96 LMSGKTFSTSPVWFLREGSMFVALGASTCSLAIATERHILMIRKRPDANKRRVF 155
 147 LLLLVAAIFMGAIVPLIGMNCINISACSLAPIYSRSLVFWYSNLMALFLMVY 205
 156 LLTGMCLIAFTGALPILGMNCINILPDCSTIPLPSKTYAF-CISIFALIVTVIL 214
 206 YLRIYVYKRTNVLSPTSGISRRRTPMKIMKTVMVVGAFVVCWPGVLVPLDGLN 265
 215 YARIYVYKSSSRKVAHNNSERS----MALFTVIVVSVFACMSPLFIILIDVA 268
 266 CR--QCGVQVHKRFFLLALINSVNPITISYKDEDMGTMKMICFSQENPE--SQE 314
 269 CRVQACPILEKQWFLVAVLSAMNPVITVLSKEMRAFFRLVCAVLRGARASPT 328
 315 NPERRPRISTVLSRSDTGSQYIED-----STSGAVCN 349
 329 QPALDPSRSKSSSSNNSHSPRYKEDLPHPDPSCTIDKNAALQNGIFCN 378

RESULT 5
 A35300
 G protein-coupled receptor edg-1 - human

C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 24-Sep-1999
C:Accession: A35300
R:HLA, T., MacLag T
J. Biol. Chem. 265, 9308-9313, 1990
A:Title: An abundant transcript induced in differentiating human endothelial cells encodes
A:Reference number: A35300; MUID:90264425; PMID:2160972
A:Accession: A35300
A:Molecule type: mRNA
A:Residues: 1-381 <HLA>
A:Cross-references: GB:M31210; NID:g181948; PIDN:AAA5236.1; PID:g181949
C:Genetics:
A:Gene: GDB:ECGF1
A:Cross-references: GDB:127754; OMIM:131222
A:Map position: 22q13-22q13
C:Superfamily: G protein-coupled receptor edg-1
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

Query Match	28.9%	Score 533.5;	DB 2;	Length 381;
Best Local Similarity	31.7%	Pred. No. 1,9e-38;		
Matches 114;	Conservative 78;	Mismatches 131;	Indels 37;	Gaps 77;

```

Oy      5 HYDKIMDPEYKRNNDYVDDMTGTGLTVILVCGEFECLIFEFSNSLVAAVYKKNFHP    64
        || :||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      28 HYN-----YGGKLNISADKNESIKLTSVET--LICCFIILENIFVLLTIKTITKFRBP    79

Oy      65 FYILLANIAAADFAGIAYVFLEMENGEVSQTLVYNNRFLROGLIDSSLTASJMLVYA    124
        || :||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      80 MYEIGINIALSDLLAGAVYTANLLLSGATTKTTPAOWFLRGSEMFVALSASFELIA    139

Oy      125 VERHMSIMRMHVSHNLTKRKRYTLILLLAWALAIFMGAPVLTCGMNCINCISACSLAPTYS    184
        || :||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      140 IERTITMLKMKLHNGSNNEFLLELISACWVISLILGGPIPMGNOCISALSOSVLYPLXH    199

Oy      185 RSYLEFWFVNSULMAFLMVYYLRIRYYVYVKRTNTLSHTS-GTSRSRRTPPKLMKYWT    243
        || :||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      200 KHIILCTFTVTPLLIVLLCYLKRSYLSLVRTRSRRLTRFKNKISKAQRSSENAWLAKTYII    259

Oy      244 VLGAFVYCWTPEGLVYLPLD-GLNCRQCQVOHYKRMYLLALANSVYNPILSYSKDEDM-Y    301
        || :||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      260 VLASVEIACMAPLEFIILLDVGCQKVYTCIDLFAEAYFLVALVANGSTNPITYLTITKEMRR    319

Oy      302 GTMKMKMIC-----EQG-----ENPRRRSRIPSPVLSKSDICS    335
        || :||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      320 AFIRISMCCCKPDSGSACKFRKPPIITAGMEFSKSCKDNSHPPCKDEGDNETMISGGVANS    379

```

PROBABLE G protein-coupled receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text-change 21-Jul-2000
 C:Accession: J01465
 R:Okazaki, H.; Ishizaka, N.; Sakurai, T.; Kurokawa, K.; Goto, K.; Kumada, M.; Takuwa, Y.
 Biochem. Biophys. Res. Commun. 190, 1104-1109, 1993
 A:Title: Molecular cloning of a novel putative G protein-coupled receptor expressed in rat
 A:Reference number: J01465; MUID:93176155; PMID:8382486
 A:Accession: J01465
 A:Molecule type: mRNA
 A:Residues: 1-352 <OK>
 A:Cross-references: GB:AB016931; NID:93445557; PIDN:BA32454.1; PID:93445558
 A:Experimental source: aortic smooth muscle
 C:Superfamily: G protein-coupled receptor edg-1
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F:35-59/Domain: transmembrane #status predicted <TM1>
 F:67-95/Domain: transmembrane #status predicted <TM2>
 F:110-128/Domain: transmembrane #status predicted <TM3>
 F:148-173/Domain: transmembrane #status predicted <TM4>
 F:190-210/Domain: transmembrane #status predicted <TM5>
 F:234-255/Domain: transmembrane #status predicted <TM6>
 F:272-293/Domain: transmembrane #status predicted <TM7>
 F:19/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:142,145, 218, 219, 329,330,331,332/Binding site: phosphate (Ser) (covalent) #status predicted

F,313/Blinding site: phosphate (Thr) (covalent) #status predicted

Query Match	27.0%	Score 499;	DB 2;	Length 352;
Best Local Similarity	33.2%	Pred. No. 1.7e-35;		
Matches 113; Conservative	69;	Mismatches 118;	Indels 40;	Gaps 9

[illegible]

RESULT 7
 A:55689
 G protein-coupled receptor 3 - human
 N:Alternate names: G protein-coupled receptor GPR3; orphan G-protein-coupled receptor
 C:Species: Homo sapiens (man)
 C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 19-May-2000
 C:Accession: A55689; S58521; C55733
 R:Ilismaa, T.P.; Klefer, J.; Liu, M.L.; Baker, E.; Sutherland, G.R.; Shine, J.
 Genomics 24, 391-394, 1994
 A>Title: Isolation and chromosomal localization of a novel human G-protein-coupled re
 A:Reference number: A55689; MUID:95213036; PMID:7658767
 A:Accession: A55689
 A:Status: preliminary
 A:Molecule type: DNA; mRNA
 A:Residues: 1-330 <IIS>
 A:Cross-references: GB:L32830; GB:L32831; NID:9602311; PIDN:AAA73560.1; PID:9602312
 R:Engerickx, D.; Denef, J.F.; Labbe, O.; Hayashi, Y.; Refetoff, B.; Vassart, G.; Patm
 Biochem. J. 309, 837-843, 1995
 A>Title: Molecular cloning of an orphan G-protein-coupled receptor that constitutivel
 A:Reference number: S58521; MUID:95366960; PMID:7639700
 A:Accession: S58521
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-330 <EGG>
 A:Cross-references: GB:X83956; NID:g1061125; PIDN:CAA56787.1; PID:g1061126
 R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsutsumi
 Genomics 23, 609-618, 1994
 A>Title: Cloning of human genes encoding novel G protein-coupled receptors.
 A:Reference number: A55733; MUID:95154831; PMID:7851889
 A:Accession: C55733
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-292 <MAR>
 A:Cross-references: GB:U13668; NID:g577416; PIDN:AAA64594.1; PID:g577417
 C:Genetics:
 A:Gene: GDB:GPR3
 A:Cross-references: GDB:371695; OMIM:600241
 A:Map position: 1p36.1-1p34.3
 C:Superfamily: melanocortin receptor
 C:Keywords: G protein-coupled receptor; transmembrane protein
 Query Match 19.0%; Score 352; DB 2; Length 330;

Best Local Similarity 30.8%; Pred. No. 7.5e-23;
Matches 96; Conservative 58; Mismatches 116; Indels 42; Gaps 11.

[illegible]

RESULT 8
S40454
G protein-coupled receptor GPCR21 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S40454
R:Saeki, Y.; Ueno, S.; Mizuno, R.; Nishimura, T.; Fujimura, H.; Nagai, Y.; Yanagihara, T.
FEBS Lett. 336, 317-322, 1993
A:Title: Molecular cloning of a novel putative G protein-coupled receptor (GPCR21) which
A:Reference number: S40454; MUID:94085630; PMID:8262253
A:Accession: S40454
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-330 <SAE>
A:Cross-references: GB:021062; NID:g455487; PIDD:BAA04641.1; PID:g455488
C:Superfamily: melanocortin receptor
C:Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein

Query Match	19.0%;	Score 351;	DB 2;	length 330;
Best Local Similarity	30.0%;	Pred. No. 9.2e-23;		
Matches 101; Conservative	61;	Mismatches 125;	Indels 50;	Gaps 12

[illegible]

RESULT 9
A33117

cannabinoid receptor CB1 - rat
C:Species: *Rattus norvegicus* (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C:Accession: A33117, C55879
R:Matilda, L.A.; Lolait, S.J.; Brownstein, M.J.; Young, A.C.; Bonner, T.I.
Nature 346, 561-564, 1990
A:Title: Structure of a cannabinoid receptor and functional expression of the cloned
A:Reference number: A33117, MUID:90332039, PMID:2165569
A:Accession: A33117
A:Molecule type: mRNA
A:Residues: 1-473 <MAT>
A:Cross-references: GB:A55812, NID:g155275, PIDD:CA93932.1, PID:g57249
R:Shire, D.; Carillon, C.; Kaghad, M.; Calandra, B.; Rinaldi-Carmona, M.; Le Fur, G.;
J. Biol. Chem. 270, 3726-3731, 1995
A:Title: An amino-terminal variant of the central cannabinoid receptor resulting from
A:Reference number: A55879, MUID:95181329, PMID:7876112
A:Accession: C55879
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SHI>
;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match	18.8%	Score 347;	DB 2;	Length 473;
Best Local Similarity	26.9%	Pred. No. 3e-22;		
Matches 80; Conservative	69;	Mismatches 122;	Indels 26;	Gaps 6;

[illegible]

RESULT 10
C17595

cannabinoid receptor CB1 - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S17595; S13668; A55879
R:Gerard, C.M.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochem. J. 279, 129-134, 1991
A:Title: Molecular cloning of a human cannabinoid receptor which is also expressed in
A:Reference number: S17595; M01D:92028798; PMID:1118258
A:Accession: S17595
A:Molecule type: mRNA
A:Residues: 1-472 <GER1>
A:Cross-references: EMBL:X54937; NID:q29914; PIDN:CAA38699.1; PID:q29915
R:Gerard, C.; Mollereau, C.; Vassart, G.; Parmentier, M.
Nucleic Acids Res. 18, 7142, 1990
A:Title: Nucleotide sequence of a human cannabinoid receptor cDNA.
A:Reference number: S13668; M01D:91088303; PMID:2263478
A:Accession: S13668
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-472 <GER2>

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 15:03:54 ; Search time 99 Seconds

(without alignments)
920.127 Million cell updates/sec

Title: US-09-581-252-14

Perfect score: 1848
Sequence: 1 MNECHYDKHMDFFYNSNTD.....GSOYIEDISGAVCNKSTS 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23:**
1: sp_archaea:**
2: sp_bacteria:**
3: sp_fungi:**
4: sp_human:**
5: sp_invertebrate:**
6: sp_mammal:**
7: sp_mhc:**
8: sp_organelle:**
9: sp_phage:**
10: sp_plant:**
11: sp_rodent:**
12: sp_virus:**
13: sp_vertebrate:**
14: sp_unclassified:**
15: sp_virus:**
16: sp_bacteriaph:**
17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1772.5	95.9	354	4	Q9NRB8
2	929	50.3	194	11	Q8VDA1
3	899	48.6	296	11	Q8VDA2
4	716.5	38.8	251	13	Q8VDA4
5	598	32.4	123	6	Q95L85
6	548	29.7	382	11	Q9R235
7	546	29.5	382	11	Q9DC35
8	544.5	29.5	326	11	Q9NR5
9	543.5	29.4	378	11	Q9Z009
10	541.5	29.3	362	13	Q8BP20
11	540.5	29.2	326	11	Q9DDK4
12	539.5	29.1	326	11	Q9NR1
13	538	29.1	326	11	Q9NR4
14	537.5	29.1	326	11	Q9NR8
15	536	29.0	326	6	Q9BF5
16	534	28.9	326	6	Q9BF48

17	533.5	28.9	326	6	Q9BF49	Q9BF49 tragelaphus
18	533.5	28.9	326	6	Q9BF47	Q9BF47 okapia john
19	532	28.8	382	4	Q9NYN8	Q9NYN8 homo sapien
20	531.5	28.8	326	6	Q9BF63	Q9BF63 octolona hy
21	531.5	28.8	326	11	Q9NR3	Q9NR3 erethizon d
22	531	28.7	326	11	Q9NR0	Q9NR0 cavia tscu
23	530.5	28.7	326	11	Q9NR7	Q9NR7 agouti tacz
24	530	28.7	326	11	Q9NR9	Q9NR9 hydrochoeru
25	530	28.7	384	13	Q9PU08	Q9PU08 fugu rubrip
26	529	28.6	326	6	Q9BF52	Q9BF52 megaptera n
27	529	28.6	326	11	Q9NR7	Q9NR7 muscardinus
28	528.5	28.6	326	11	Q9NR8	Q9NR8 castor cana
29	528	28.6	326	6	Q9BF70	Q9BF70 trichechus
30	528	28.6	326	6	Q8MK88	Q8MK88 amblyosomus
31	528	28.6	326	6	Q9BF67	Q9BF67 macroscellid
32	528	28.6	326	6	Q9BF66	Q9BF66 elephantulu
33	527.5	28.5	326	6	Q9BF50	Q9BF50 hippopotamu
34	526.5	28.5	326	6	Q8MK87	Q8MK87 tadarida dr
35	525	28.4	326	6	Q9BF45	Q9BF45 ceratotheri
36	524.5	28.4	326	6	Q9BF76	Q9BF76 tamandua te
37	523.5	28.3	326	6	Q9BF46	Q9BF46 equus cabal
38	523.5	28.3	326	6	Q9BF57	Q9BF57 hylobates c
39	523.5	28.3	326	6	Q9BF72	Q9BF72 sorex arane
40	523	28.3	326	6	Q9BF69	Q9BF69 procavia ca
41	522	28.2	325	11	Q9NR9	Q9NR9 tamias stri
42	521	28.2	326	6	Q9BF75	Q9BF75 myrmecophag
43	521	28.2	326	6	Q9BF73	Q9BF73 condylura c
44	520.5	28.2	326	6	Q9BF44	Q9BF44 tapirus ind
45	520	28.1	326	6	Q9BF60	Q9BF60 lemur calta

ALIGNMENTS

RESULT 1

ID	Q9NRB8	PRELIMINARY:	PRT:	354 AA.
AC	Q9NRB8;			
DT	01-OCT-2000 (TRENBLREL. 15, Created)			
DI	01-OCT-2000 (TRENBLREL. 15, Last sequence update)			
DT	01-MAR-2003 (TRENBLREL. 23, Last annotation update)			
DE	G-protein coupled receptor EDG-7.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20351181; PubMed=10891327;			
RA	Fitzgerald L.R., Dytko G.M., Sarau H.M., Mannan I.J., Ellis C.,			
RA	Lane P., Tan K.B., Wilson S., Bergsma D.J., Ames R.S., Foley J.J.,			
RA	Cambell D., McMillan L., Evans N., Elshourbagy N., Tsui P.,			
RT	"Identification of an EDG7 Variant, HOFN30, a G-Protein-Coupled			
RT	Receptor for Lysophosphatidic Acid."			
RL	Biochem. Biophys. Res. Commun. 273:805-810(2000).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL: AF236117; AAF91291.1; -			
DR	InterPro: IPR005385; EDG7_receptor.			
DR	InterPro: IPR00276; GPCR_Rhodopsn.			
DR	InterPro: IPR004065; LPAR_receptor.			
DR	Pfam: PF00001; 7tm_1; 1.			
DR	PRINTS: PR01560; EDG7RECEPTOR.			
DR	PRINTS: PR00237; GPCR_RHODOPSIN.			
DR	PRINTS: PR01527; LPARRECEPTOR.			
DR	PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.			
KW	G-protein coupled receptor; Receptor; Transmembrane.			
SO	SEQUENCE 354 AA; 40339 MW; A70EDSCFAAF7D706 CRC64;			

Query Match 95.9%; Score 1772.5; DB 4; Length 354;
Best Local Similarity 96.0%; Pred. No. 4e-149;
Matches 340; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

```

QY 1 MNECHDKHMDFFYNSNTDVTVDWGTGKLVLCVGTFFCLFIFFSNSLVAIVIKNRK 60
DB 1 MNECHDKHMDFFYNSNTDVTVDWGTGKLVLCVGTFFCLFIFFSNSLVAIVIKNRK 60
QY 61 HFFPYLLANLAADFFAGIAVFLMNTGPNVSKITLVNRMFLRQGLDSSLTASLTNL 120
DB 61 HFFPYLLANLAADFFAGIAVFLMNTGPNVSKITLVNRMFLRQGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLGNCLNISACSSLA 180
DB 121 LVIAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLGNCLNISACSSLA 180
QY 121 LVIAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLGNCLNISACSSLA 180
DB 121 LVIAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLGNCLNISACSSLA 180
QY 181 PIYSRSLVFWTVSNLMAFLIMVYVYLRIVYVYKRTNVLSPHTSGSISRRRTPMKLMKT 240
DB 181 PIYSRSLVFWTVSNLMAFLIMVYVYLRIVYVYKRTNVLSPHTSGSISRRRTPMKLMKT 240
QY 241 VMTVLAFAVVCWTPGLVLLDGLNCGCVQVHKRWFLLALLNSVYVNIYSKDEDM 300
DB 241 VMTVLAFAVVCWTPGLVLLDGLNCGCVQVHKRWFLLALLNSVYVNIYSKDEDM 300
QY 301 YGTMKKICCFSOE-NPERRSRIPSTVLSRSDPTGSOYIEDSISOGAVCNKSTS 353
DB 301 YGTMKKICCFSOE-NPERRSRIPSTVLSRSDPTGSOYIEDSISOGAVCNKSTS 353

```

RESULT 2

```

Q8VD41 ID 08VD41 PRELIMINARY; PRT; 194 AA.
AC 08VD41:
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Endothelial differentiation G-protein-coupled receptor 7
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Myenteric plexus;
RA Segura B.J., Xiao L.-Q., Cowles R.A., Logsdon C.D., Mulholland M.W.;
RT "LPA Mediates Calcium Signaling in Enteric Gila.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY013709; AAK07694.1;
DR InterPro: IPR005385; EDG7_Receptor.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR InterPro: IPR004065; LPareceptor.
PFam: PF00001; 7tm_1; 1.
PRINTS: PRO1560; EDG7/RECEPTOR.
PRINTS: PRO0237; GPCR/RHODOPSIN.
DR PRINTS: PRO1527; LPARECEPTOR.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT SEQUENCE 194 AA; 22343 MW; 920D1CCB596F1B8 CRC64;
SQ

```

Query Match 50.3%; Score 929; DB 11; Length 194;

Best Local Similarity 90.2%; Pred. No. 1,4e-74;

Matches 175; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

```

QY 128 HMSIMRHRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLGNCLNISACSSLA 187
DB 128 HMSIMRHRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLGNCLNISACSSLA 187
QY 188 LVIAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLGNCLNISACSSLA 247
DB 188 LVIAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLGNCLNISACSSLA 247
QY 248 FVVCWTPGLVLLDGLNCGCVQVHKRWFLLALLNSVYVNIYSKDEDMYGTMKM 307
DB 248 FVVCWTPGLVLLDGLNCGCVQVHKRWFLLALLNSVYVNIYSKDEDMYGTMKM 307

```

```

DB 121 FVVCWTPGLVLLDGLNCGCVQVHKRWFLLALLNSVYVNIYSKDEDMYGTMKM 180
QY 308 ICFWQESNPEROPS 194
DB 181 ICFWQESNPEROPS 194

```

RESULT 3

```

Q8VD42 ID 08VD42 PRELIMINARY; PRT; 296 AA.
AC 08VD42:
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Endothelial differentiation G-protein-coupled receptor 2
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Myenteric plexus;
RA Segura B.J., Xiao L.-Q., Cowles R.A., Logsdon C.D., Mulholland M.W.;
RT "LPA Mediates Calcium Signaling in Enteric Gila.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DE EMBL: AY013708; AAK07693.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR InterPro: IPR004065; LPareceptor.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO0237; GPCR/RHODOPSIN.
DR PRINTS: PRO1527; LPARECEPTOR.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT SEQUENCE 296 AA; 33972 MW; F71EA0267D0275A3 CRC64;
SQ

```

Query Match 48.6%; Score 899; DB 11; Length 296;

Best Local Similarity 54.2%; Pred. No. 9.6e-72;

Matches 162; Conservative 70; Mismatches 63; Indels 4; Gaps 3;

```

QY 3 ECHYDKHMDFFYNSNTDVTVDWGTGKLVLCVGTFFCLFIFFSNSLVAIVIKNRK 61
DB 3 ECHYDKHMDFFYNSNTDVTVDWGTGKLVLCVGTFFCLFIFFSNSLVAIVIKNRK 61
QY 62 HFFPYLLANLAADFFAGIAVFLMNTGPNVSKITLVNRMFLRQGLDSSLTASLTNL 121
DB 62 HFFPYLLANLAADFFAGIAVFLMNTGPNVSKITLVNRMFLRQGLDSSLTASLTNL 121
QY 122 LVIAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLGNCLNISACSSLA 181
DB 122 LVIAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLGNCLNISACSSLA 181
QY 182 IYSRSLVFWTVSNLMAFLIMVYVYLRIVYVYKRTNVLSPHTSGSISRRRTPMKLMKT 241
DB 182 IYSRSLVFWTVSNLMAFLIMVYVYLRIVYVYKRTNVLSPHTSGSISRRRTPMKLMKT 241
QY 242 MYVLAFAVVCWTPGLVLLDGLNCGCVQVHKRWFLLALLNSVYVNIYSKDEDM 300
DB 242 MYVLAFAVVCWTPGLVLLDGLNCGCVQVHKRWFLLALLNSVYVNIYSKDEDM 300
QY 239 VIVGAFAVVCWTPGLVLLDGLNCGCVQVHKRWFLLALLNSVYVNIYSKDEDM 296
DB 239 VIVGAFAVVCWTPGLVLLDGLNCGCVQVHKRWFLLALLNSVYVNIYSKDEDM 296

```

RESULT 4

```

Q8OFL4 ID 08OFL4 PRELIMINARY; PRT; 251 AA.
AC 08OFL4:
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

```

```

DE SC:d22B13.1 (Novel protein similar to lysophosphatidic acid receptor)
DE (Fragment).
GN SC:d22B13.1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Babbage A.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL; AL603747; CAD24409.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
DR G-Protein coupled receptor; Receptor; Transmembrane.
NM NON_TER 1
NM NON_TER 1
SQ SEQUENCE 251 AA; 29076 MW; C4671873B7D5F03 CRC64;

Query Match 38.8%; Score 716.5; DB 13; Length 251;
Best Local Similarity 51.6%; Pred. No. 1.2e-55;
Matches 126; Conservative 60; Mismatches 55; Indels 3; Gaps 2;

QY 3 ECHYDKHDFEYNSRNTVDWNG-TKLIVLCVGFECLEIFPNSLVIAVAKNKF 61
DB 10 QCYNETAEFYNSOKLTATEMANVSKLVKGL-GIVVCIFMLANLVIAVYINRF 67
QY 62 HPEFYLLANLAADFAGIAVFLMFTGPKSKITLVNRMFLROGLDSSLTASLTNL 121
DB 68 HPEFYLLANLAADFAGIAVFLMFTGPKSKITLVNRMFLROGLDSSLTASLTNL 127
QY 122 VIAVERHMSIMRNVSHLTKRVTLLILVMALEFNGAVFTLGNCLNISACSLAP 181
DB 128 AIAIERHITVFMQIHTMSNRNVVYVIVITMSIVGALPSVGMNCICAIDTCSNAP 187
QY 182 IYSRSYLVFTVNSNMAFLIVVYLVRIYVYVKKRTNLSPTSGSSISRRPMLMTV 241
DB 188 LYSNSYLGFMALFNLYTVVVAHLVLAHFMVYRQRTMRSRSGQRNRDITMSLKTV 247
QY 242 MTVL 245
DB 248 VIVL 251.

RESULT 5
Q95L85 PRELIMINARY; PRT; 123 AA.
AC Q95L85;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Endothelial differentiation gene 7 protein (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang D.-A.; Tiyyl G.; Watsky M.A.;
RT "EDG7 of rabbit";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC EMBL; AF04276; AAL01883.1; -.
DR InterPro: IPR005385; EDG7_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR01360; EDG7_RECEPTOR.

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DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 123 AA; 13883 MW; EB16BAFA7105B65 CRC64;

Query Match 32.4%; Score 598; DB 6; Length 123;
Best Local Similarity 97.5%; Pred. No. 1.9e-45;
Matches 116; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 17 SNTDVTDDMTGKTLIVLCVGFECLEIFPNSLVIAVAKNKFHFPFYLLANLAAD 76
DB 4 SNTDVTDDMTGKTLIVLCVGFECLEIFPNSLVIAVAKNKFHFPFYLLANLAAD 63
QY 77 PFAGIAVFLMFTGPKSKITLVNRMFLROGLDSSLTASLTNLVIAVERHMSIMRNV 135
DB 64 PFAGIAVFLMFTGPKSKITLVNRMFLROGLDSSLTASLTNLVIAVERHMSIMRNV 122

RESULT 6
Q9R235 PRELIMINARY; PRT; 382 AA.
AC Q9R235;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Lysophospholipid receptor BL.
NM EDG1 OR Lep1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-1295VJ;
RA MEDLINE-99132320; PubMed-9931453;
RA Zhang G., Contos J.J., Weiner J.A., Fukushima N., Chun J.;
RT *Comparative analysis of three murine G-protein coupled receptors
RT activated by sphingosine-1-phosphate.*;
RL Gene 227:89-99(1999).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC EMBL; AF108019; AAD16975.1; -.
DR MGD: MGI:1096355; Edg1.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR004061; S1P_receptor.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PRINTS: PR01523; S1PRECEPTOR.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 382 AA; 42613 MW; 2EE4B974E9FB39C CRC64;

Query Match 29.7%; Score 548; DB 11; Length 382;
Best Local Similarity 34.2%; Pred. No. 1.7e-40;
Matches 117; Conservative 79; Mismatches 126; Indels 20; Gaps 7;

QY 27 GTKLIVLCVGFECLEIFPNSLVIAVAKNKFHFPFYLLANLAADFAGIAVFL 86
DB 44 GIKLSVYFI--LICCFILLENIFVLITWKTKRHPMYTYIGNALSDLAGAVAYAN 101
QY 87 MENTGPKSKITLVNRMFLROGLDSSLTASLTNLVIAVERHMSIMRNVSNLTKRVT 146
DB 102 LLSGATYTKLTPAQMFLREGSMFVALSAYFSLAIAIERITMLKKLHNGSNSRSF 161
QY 147 LILILVMAIFMGAVPTLGNWCLNISACSLATVRSYVFTVSNLMAFLMNVYV 206
DB 162 LILSACWYISLIGLPSMGWNCISSCSCTVLPDKRHVILFCTVFTLLSLIVLY 221
QY 207 LRIYVYVRKTNVLSPHTSISRRRT--PKLTKVTMTVLGAFVVCWTPGLVVLPLD-G 263

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Db      222 CRIYSLVRTSRRLTFEKNKNSKASRSSEKSLALTKYIIVLSYFIACMAFLILLDVG 281
Qy      264 LNCRCGVQVHKRFFLLALLNSVYVNPITISYKDEDMYGTMKKMICFSGENPE-----R 318
Db      282 CKAATCDILYKAEFFVLAVLNSGTNPITITLTKKERRAFIRIVSCCKPNDGSAGKFK 341
Qy      319 RPSRIPSTVLSR--SDTGSQYIEDS-----ISQAVCNKS 351
Db      342 RPI-IPGMEFRSRKSDNSHPQKDDGNPPTIMSGVNSS 382

RESULT 7
ID      09DC35      PRELIMINARY;      PRT;      382 AA.
AC      09DC35;
DT      01-JUN-2001 (TREMBlrel. 17, Created)
DT      01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DB      Endothelial differentiation sphingolipid G-protein-coupled receptor
        1.
        EDG1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Lung;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Mishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA      Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA      Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schirra L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA      Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA      Hayashizaki Y.;
RA      *Functional annotation of a full-length mouse cDNA collection.*;
RA      Nature 409:685-690(2001).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DB      EMBL: AK004591; BAB23393.1; -.
DB      MGI:1096355; Edg1.
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      InterPro: IPR004061; S1Preceptor.
DR      Pfam: PF00001; 7tm_1.1.
DR      PRINTS: PR00237; GPCRHHODOPS.
DR      PRINTS: PR01523; S1PRECEPTOR.
DR      PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR      PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW      G-protein coupled receptor; Receptor; Transmembrane.
SQ      SEQUENCE 382 AA; 42639 MW; 5FE4C9A2BD65CB2A CRC64;

Query Match      29.5%; Score 546; DB 11; Length 382;
Best Local Similarity 34.2%; Pred. No. 2.5e-40;
Matches 117; Conservative 76; Mismatches 127; Indels 20; Gaps 7;

Qy      27 GTRKIVLYCAGTFCLEFFFSNSLVIAVYKRNKFFPPFYLLANLAADFPAGIAYVEL 86
Db      44 GIKLTVSVFL--LTCGFIILNFIYLLITKTKFHHFPMYFIGNLALSDLAGAVATYAN 101
Qy      87 MENTGVSKTLTVNRMFLRGLDSSLTASLTNLTVAVERHMSIMMRVHSNLTTRKRYT 146

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Db      102 LLLSGATYKLTLPQWFLREGSMFVALSASFSLAIAIRYITMLKMKLHNGSNSRSF 161
Qy      147 LLLLVVAIAIFMGAVFTLGMNCINISACSSLAIPYSRYVWYVSNLMAFLIMVYV 206
Db      162 LLLISACVVISLILGGLIMGMNCISLSSCSTVPLHKHKLITCTVFTVLLLSIYLY 221
Qy      207 LRIYVYVKKRTNVLSPHTSGSISRRT--PMKLMKRVYVVGAFVVCWPTGLVPLD-G 263
Db      222 CRIYSLVRTSRRLTFEKNKNSKASRSSEKSLALTKYIIVLSYFIACMAFLILLDVG 281
Qy      264 LNCRCGVQVHKRFFLLALLNSVYVNPITISYKDEDMYGTMKKMICFSGENPE-----R 318
Db      282 CKAATCDILYKAEFFVLAVLNSGTNPITITLTKKERRAFIRIVSCCKPNDGSAGKFK 341
Qy      319 RPSRIPSTVLSR--SDTGSQYIEDS-----ISQAVCNKS 351
Db      342 RPI-IPGMEFRSRKSDNSHPQKDDGNPPTIMSGVNSS 382

RESULT 8
ID      099NR5      PRELIMINARY;      PRT;      326 AA.
AC      099NR5;
DT      01-JUN-2001 (TREMBlrel. 17, Created)
DT      01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      EDG1 (Fragment).
GN      EDG1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21082082; PubMed=11214319;
RA      Murphy W.C., Elzirik E., Johnson W.B., Zhang Y.P., Ryder O.A.,
RA      O'Brien S.J.;
RA      *Molecular phylogenetics and the origins of placental mammals.*;
RA      Nature 409:614-618(2001).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DB      EMBL: AY011706; AK01975.1; -.
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      InterPro: IPR004061; S1Preceptor.
DR      Pfam: PF00001; 7tm_1.1.
DR      PRINTS: PR00237; GPCRHHODOPS.
DR      PRINTS: PR01523; S1PRECEPTOR.
DR      PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR      PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW      G-protein coupled receptor; Receptor; Transmembrane.
FT      NON_TER 1
FT      NON_TER 326
SQ      SEQUENCE 326 AA; 36574 MW; 7B6DF34BD398B17 CRC64;

Query Match      29.5%; Score 544.5; DB 11; Length 326;
Best Local Similarity 35.1%; Pred. No. 2.9e-40;
Matches 110; Conservative 75; Mismatches 117; Indels 11; Gaps 5;

Qy      27 GTRKIVLYCAGTFCLEFFFSNSLVIAVYKRNKFFPPFYLLANLAADFPAGIAYVEL 86
Db      4 GIKLTVSVFL--LTCGFIILNFIYLLITKTKFHHFPMYFIGNLALSDLAGAVATYAN 61
Qy      87 MENTGVSKTLTVNRMFLRGLDSSLTASLTNLTVAVERHMSIMMRVHSNLTTRKRYT 146
Db      62 LLLSGATYKLTLPQWFLREGSMFVALSASFSLAIAIRYITMLKMKLHNGSNSRSF 121
Qy      147 LLLLVVAIAIFMGAVFTLGMNCINISACSSLAIPYSRYVWYVSNLMAFLIMVYV 206
Db      122 LLLISACVVISLILGGLIMGMNCISLSSCSTVPLHKHKLITCTVFTVLLLSIYLY 181
Qy      207 LRIYVYVKKRTNVLSPHTSGSISRRT--PMKLMKRVYVVGAFVVCWPTGLVPLD-G 263

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DB 182 CRISLVTRSRRLTFRNKNISKASSSEKSLALKTIVIVLSVFIACNAPLIFILLIDVVG 241
 QY 264 INCRQCGYQVHKRWFLALLNSVNPPIIYSKYDEDMGTMKMKICFSGQENPE-----R 318
 DB 242 CKAQCDLTKAEYFLVALVANSNGINPIITITNEMKRAFRIRYSCCKCPGSDSNGKFK 301
 QY 319 RPSRIPSTVLSRS 331
 DB 302 RPI-IPGMEFSRS 313

RESULT 9

Q92009 PRELIMINARY; PRT; 378 AA.
 ID Q92009;
 AC Q92009;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE LYSPHOSPHOLIPID receptor B3 (Endothelial differentiation).
 NP LPB3 OR EDG3.
 NC Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SVJ;
 RX MEDLINE=99132320; PubMed=9931453;
 RA Zhang G., Contos J.J.A., Weiner J.A., Fukushima N., Chun J.;
 RT "Comparative analysis of three murine G-protein coupled receptors
 RL activated by sphingosine-1-phosphate.";
 RL Gene 227:89-99(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ohta K., Wada A., Igarashi Y.;
 RT "Mus musculus sphingosine 1-phosphate receptor Edg3 gene, complete.";
 RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, Head, Lung, and Testis;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;
 RA "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AF108021; AAD1697.1;
 DR EMBL; AB028143; BAA78207.1;
 DR EMBL; AK028043; BAC25715.1;
 DR EMBL; AK029852; BAC26645.1;
 DR EMBL; AK030134; BAC26800.1;
 DR EMBL; AK047268; BAC33008.1;
 DR EMBL; AK081919; BAC38373.1;
 DR EMBL; AK084944; BAC39316.1;
 DR EMBL; AK085180; BAC39383.1;
 DR MGI; MGI:1339365; Edg3.
 DR InterPro: IPR000194; ATPase_a/bcentre.
 DR InterPro: IPR004062; EDG3_receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR004061; S1Preceptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO1524; EDG3RECEPTOR.
 DR PRINTS; PRO0237; GPCR_RHODOPSIN.
 DR PRINTS; PRO1523; S1PRECEPTOR.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
 DR PROSITE; PS00337; G_PROTEIN_RECEPTOR; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEPTOR; 1.
 KW Receptor.
 SQ SEQUENCE 378 AA; 42270 MW; F46B25E77ECDC8 CRC64;

Query Match 29.4%; Score 543.5; DB 11; Length 378;
 Best Local Similarity 35.2%; Pred. No. 41e-40;
 Matches 123; Conservative 66; Mismatches 123; Indels 37; Gaps 9;

QY 27 GTRIVILCVGTFFCLFFFSNSLVIAVIRKRRKFFPYLLANLAADPAGIAYVL 86
 DB 39 GLTITLIELVY--CSFYLENLAMVLAIRKKNKRNRRFFIGNALCDLLAGIATKYN 96
 QY 87 MENTGPVSKTLTVNRMFLRQGLDSSLTASLTNLVIAVERMSIRMRHSNLTTRKRYT 146
 DB 97 ILMGRKTFEISLPVWFLEEGSMFVALGASTCSLTAIAIERHLTMKRPYDANKKHRYF 156
 QY 147 LILILVMAIIFMGAVPTIGMNCINISGSSLAPIYSKYLVFTVSNLMAFLI-MVVV 205
 DB 157 ILIGMCWLIASFGLALPIIGMNCLENFDPDCTILPLYSKRYIAF-LISIFTAIVTVIL 215
 QY 206 YLRIVVYVRKTVNSPHTSGSISRRRPMTKMTVMYVLAFAVVCWPGVLVPLDGN 265
 DB 216 YARITCIYKSSSRRAVANHNS-----ERSMALLRIVVIVSYFIACWSP-LTILFLIDVA 268
 QY 266 CR--OCGVOHVRKRWFLALLNSVNPPIIYSKYDEDMGTMKMKIC-CF-----SOE 314
 DB 269 CKAQCDLTKAEYFLVALVANSAMPVITYTLASKEMRRAPFRLVCGCLVKGKGTQASPM 328
 QY 315 NERRRPSRIPSTVLSRSDTGSQYID-----SISGAVC 348
 DB 329 QPALDPSNRKSSSSNNSSHSPVKEDLPVATSCITIDKNRSPONGVLC 377

RESULT 10

Q8BP20 PRELIMINARY; PRT; 378 AA.
 ID Q8BP20;
 AC Q8BP20;
 DT 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Endothelial differentiation.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;
 RA "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK078443; BAC3727.1;
 DR MGI; MGI:42339 MW; F416D8BE7727BDC8 CRC64;
 SQ SEQUENCE 378 AA; 42339 MW; F416D8BE7727BDC8 CRC64;

Query Match 29.3%; Score 541.5; DB 11; Length 378;
 Best Local Similarity 35.2%; Pred. No. 6.2e-40;
 Matches 123; Conservative 65; Mismatches 124; Indels 37; Gaps 9;
 QY 27 GTRIVILCVGTFFCLFFFSNSLVIAVIRKRRKFFPYLLANLAADPAGIAYVL 86
 DB 39 GLTITLIELVY--CSFYLENLAMVLAIRKKNKRNRRFFIGNALCDLLAGIATKYN 96
 QY 87 MENTGPVSKTLTVNRMFLRQGLDSSLTASLTNLVIAVERMSIRMRHSNLTTRKRYT 146
 DB 97 ILMGRKTFEISLPVWFLEEGSMFVALGASTCSLTAIAIERHLTMKRPYDANKKHRYF 156
 QY 147 LILILVMAIIFMGAVPTIGMNCINISGSSLAPIYSKYLVFTVSNLMAFLI-MVVV 205
 DB 157 ILIGMCWLIASFGLALPIIGMNCLENFDPDCTILPLYSKRYIAF-LISIFTAIVTVIL 215
 QY 206 YLRIVVYVRKTVNSPHTSGSISRRRPMTKMTVMYVLAFAVVCWPGVLVPLDGN 265
 DB 216 YARITCIYKSSSRRAVANHNS-----ERSMALLRIVVIVSYFIACWSP-LTILFLIDVA 268
 QY 266 CR--OCGVOHVRKRWFLALLNSVNPPIIYSKYDEDMGTMKMKIC-CF-----SOE 314
 DB 269 CKAQCDLTKAEYFLVALVANSAMPVITYTLASKEMRRAPFRLVCGCLVKGKGTQASPM 328

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OY 315 NPERPRIPSTVLSRSDTGSQYED-----SISGAVC 348
DB 329 QPALDPSRKSSSSNNSSHPKVEDLPVATSSCIIDKNRSFQNGVLC 377

RESULT 11
O9DDK4 PRELIMINARY; PRT; 362 AA.
AC Q9DDK4;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Sphingosine 1-phosphate receptor.
GN EDG1.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;

[1]
SEQUENCE FROM N.A.
RX MEDLINE=20563813; PubMed=11112429;
RA Im D.S., Ungar A.R., Lynch K.R.;
RT "Characterization of a zebrafish (Danio rerio) sphingosine 1-phosphate
RL receptor expressed in the embryonic brain.";
RL Biochem. Biophys. Res. Commun. 279:139-143(2000).
DR EMBL; AF321294; AAC45430.1; -.
DR ZFIN; ZDB-GENE-001228-2; edg1.
DR InterPro; IPR000276; GPCR_Rhodpn.
DR InterPro; IPR004061; S1PReceptor.
DR Pfam; PF00003; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KM Receptor.
SQ SEQUENCE 362 AA; 40583 MW; 43A398871DA2D9D4 CRC64;

Query Match 29.28; Score 540.5; DB 13; Length 362;
Best Local Similarity 35.08; Pred. No. 7.3e-40;
Matches 115; Conservative 68; Mismatches 127; Indels 19; Gaps 6;

OY 41 CLTIFFNSIVIAVINKRHFPPFYLLANLAADFFAGIAYVFLMNTGSPVSKITLVN 100
DB 35 CCEIILENVLLTITWTKRFRPMYFIGNLSDLAGVYVYANILLSGANTYKILPT 94
OY 101 RMFLROGLDSSILFASLTNLLVAVERRHMSIMRVRHNSLTKRVTLLILLVAIATMG 160
DB 95 QMFPRBSMVALAASFSLAIAIERHILMLKHLNNGKTCVFMILSTWFIATILG 154
OY 161 AVPLIGMNCISNACSISLAPIYSRSYLVFTVSNMAFLIMVVYLYIVYVYKRTNVL 220
DB 155 GLPMVGNICIDISNCGSTVPLVHKAYILFCTYFESVILMAIVLYAIRYALVATRSRKL 214
OY 221 -----SPRTSSISRRRTPMLAKTVYVLCGFVVCWTPGLVYLPLDLGNCR--QCGVQHV 274
DB 215 VFRKVAAGRSNKSSEKSMALLITVILVLSCTIACWAPLFLILLD--VACQTLTCSITVY 273
OY 275 KRMFLALATNSVYVNPPIIYSYKDEDMYGTMKMKICCSQENPERRPSR-IPSTVLSR--S 331
DB 274 AEFMALAVLANSANPLITLITLSEMRARAFIKMLNCGVCVQPSGKSRPIMGAEFSRKS 333
OY 332 DTGSQYIEDS-----ISGAVCNKS 351
DB 334 DNSSHPKDEPEYSPRETIYSSGNITSS 362

RESULT 12
O99NR1 PRELIMINARY; PRT; 326 AA.
AC Q99NR1;
DT 01-JUN-2001 (Tremblrel. 17, Created)

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DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE EDG1 (Fragment).
GN EDG1.
OS Heterocephalus glaber (Naked mole-rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Bathyergidae;
OC Heterocephalus.
NCBI_TaxID=10181;
RN [1]
RX SEQUENCE FROM N.A.
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AY011711; AK01979.1; -.
DR InterPro; IPR000276; GPCR_Rhodpn.
DR InterPro; IPR004061; S1PReceptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KM G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT TER 326
SQ SEQUENCE 326 AA; 36607 MW; A0716ADF7BF5BA6 CRC64;

Query Match 29.28; Score 539.5; DB 11; Length 326;
Best Local Similarity 34.08; Pred. No. 8e-40;
Matches 112; Conservative 77; Mismatches 117; Indels 23; Gaps 6;

OY 27 GTKIVYLCVGTFFCLIFFSNSIVIAVINKRHFPPFYLLANLAADFFAGIAYVFL 86
DB 4 GIKLTIVVFI--LICFTIILENIFVLLTWTKRFRPMYFIGNLSDLAGVAVYAN 61
OY 87 MFTGPAVSKITLVNRMFLROGLDSSILFASLTNLLVAVERRHMSIMRVRHNSLTKRVT 146
DB 62 LLSGATYTKITLPAQWFLREGSMVALSASFSLAIAIERYITMLKHLNNGSSRSF 121
OY 147 LLLILVAIAIFMGAVPLIGMNCISNACSISLAPIYSRSYLVFTVSNMAFLIMVVY 206
DB 122 LLISACWVILILGLLIMGMNCISLSQSTVPLVHKAYILFCTVFTLLIATVILY 181
OY 207 LRIYVYKRTNVLSPRTSSISRRRT--FMKLKTVYVLCGFVVCWTPGLVYLPLD-G 263
DB 182 CRYSILVTRTSRRTFRKRNISKASRSSEKSLALIKTVILVSVFIACWAPLFLILLDVG 241
OY 264 LNCRCGVQHVKKRMFLALATNSVYVNPPIIYSYKDEDMYGTMKMKICCSQENPE-----R 318
DB 242 CKYKTCILTKAEFLVLAIVNSGTNPITLTINKERRAFIRIMSCCKPMDSTGKIK 301
OY 319 RP-----SRIPSTVLSRSDTGSQYIED 340
DB 302 RPIIAGMEFSR-----SKSDNSHPKOD 324

RESULT 13
O99NR4 PRELIMINARY; PRT; 326 AA.
AC Q99NR4;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE EDG1 (Fragment).
GN EDG1.
OS Hystrix brachyurus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Hystriidae; Hystrix.
NCBI_TaxID=143286;

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[1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE-21082082; PubMed-11214319;
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 RT O'Brien S.J.;
 RL "Molecular phylogenetics and the origins of placental mammals.";
 CC Nature 409:614-618(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AY011708; AAK01976.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR004061; S1Preceptor.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON_TER 1 326
 FT SEQUENCE 326 AA; 36546 MW; 3E66CA765F725BA9 CRC64;

Query Match 29.1%; Score 538; DB 11; Length 326;
 Best Local Similarity 36.1%; Pred. No. 1.1e-39;
 Matches 104; Conservative 73; Mismatches 105; Indels 6; Gaps 4;

QY 27 GTKLIVYCVGTFPCLEFFFSNSLVIAVINKRKHFFPYLLNLAAADFFAGIAYVEL 86
 DB 4 GIKLTIVYVFI--LICCFILLENVFLVLTMTKTKRHRPMYFICGLALSDLAGAYTAN 61
 QY 87 MENTGPSKTLTVNRMFLRQGLDSSLTASLTNLVIAVERHMSIMRKHVSNTLTKRYT 146
 DB 62 LLISGATYKTLTPAQMFREGSMFVALSASFSLALAIERYITMLKMLHNGSNSSRF 121
 QY 147 LLLILVMAIAFMGAVPLIGNCLNLSACSSLIAPISRSYLVFTVSNLMAFLIMVYV 206
 DB 122 LLISACWVLSILGLPLTMGMNCLSSSCSTVPLVHKHYTLFCTVFTLLLAIVLY 181
 QY 207 LRIYVYVYKRTNVLSPHTSGSISRRT--PMKIMKTVMVIGAFVWCWTPGLVPLD-G 263
 DB 182 CRYSVLTFRSRRLTFKRNISAKSSSEKSLALTKYIIVLSVFIACAPLFIILLDVG 241
 QY 264 LNCRCGVQVHYKRMFLALALNSVNPPIYSKEDM-YGTMKKMICC 310
 DB 242 CKVKTCIDILYKAEFLVLAIVNSGTPPIYTLTNKEMRRAPTRIMSCC 289

RESULT 14

Q99N08 PRELIMINARY; PRT; 326 AA.

Q99N08; [1]
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE EDG1 (Fragment).
 GN GN
 OS Myocastor coypu (Coypu) (Nutria).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognath; Myocastoridae;
 OC Myocastor.
 OC NCBI_TaxID=10157;
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21082082; PubMed-11214319;
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 RT O'Brien S.J.;
 RL "Molecular phylogenetics and the origins of placental mammals.";
 CC Nature 409:614-618(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AY011714; AAK01982.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR004061; S1Preceptor.

DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PRINTS: PR01523; S1PRECEPTOR.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON_TER 1 326
 FT SEQUENCE 326 AA; 36357 MW; 18963183FB9742FF CRC64;

Query Match 29.1%; Score 537.5; DB 11; Length 326;
 Best Local Similarity 35.4%; Pred. No. 1.2e-39;
 Matches 102; Conservative 75; Mismatches 106; Indels 5; Gaps 3;

QY 26 TGTKLIVYCVGTFPCLEFFFSNSLVIAVINKRKHFFPYLLNLAAADFFAGIAYVE 85
 DB 3 SCVKLTIVYVFI--LICCFILLENVFLVLTMTKTKRHRPMYFICGLALSDLAGAYTAN 60
 QY 86 LMENTGPSKTLTVNRMFLRQGLDSSLTASLTNLVIAVERHMSIMRKHVSNTLTKRY 145
 DB 61 NLLSGTYYRLTLVQWFLREGSMFVALSASFSLALAIERYITMLKMLHNGSNSSRF 120
 QY 146 TLLILVMAIAFMGAVPLIGNCLNLSACSSLIAPISRSYLVFTVSNLMAFLIMVY 205
 DB 121 FLLISGCAVLSILGLPLTMGMNCLVDPSCSTVPLVHKHYTLFCTVFTLLLAIVLY 180
 QY 206 LRIYVYVYKRTNVLSPHTSGSISRRT--PMKIMKTVMVIGAFVWCWTPGLVPLD- 262
 DB 181 YCRISLVTRSRRLTFKRNISAKSSSEKSLALTKYIIVLSVFIACAPLFIILLDVG 240
 QY 263 GLNCRQGVQVHYKRMFLALALNSVNPPIYSKEDM-YGTMKKMICC 310
 DB 241 GCKVTCIDILYKAEFLVLAIVNSGTPPIYTLTNKEMRRAPTRIMVSC 288

RESULT 15

Q9BF65 PRELIMINARY; PRT; 326 AA.

Q9BF65; [1]
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE EDG1 (Fragment).
 GN GN
 OS Oryzteropus afer (Aardvark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Tubulidentata; Oryzteropodidae; Oryzteropus.
 OC NCBI_TaxID=9818;
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21082082; PubMed-11214319;
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 RT O'Brien S.J.;
 RL "Molecular phylogenetics and the origins of placental mammals.";
 CC Nature 409:614-618(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AY011701; AAK01970.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR004061; S1Preceptor.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PRINTS: PR01523; S1PRECEPTOR.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON_TER 1 326
 FT SEQUENCE 326 AA; 36562 MW; 6946C83CBD79D715 CRC64;

Query Match 29.0%; Score 536; DB 6; Length 326;
 Best Local Similarity 36.8%; Pred. No. 1.6e-39;
 Matches 106; Conservative 69; Mismatches 107; Indels 6; Gaps 4;

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OM protein - protein search, using SW model

Run on: August 18, 2003, 15:09:56 : Search time 30 Seconds
(without alignments)
497.858 Million cell updates/sec

Title: US-09-581-252-14

Perfect score: 1848

Sequence: 1 MNECHYDKHMDFFYRNSNTD.....GSQYIEDSISGAVCNKSTS 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Dackfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1848	100.0	353	3	US-08-997-803-14
2	1838	99.5	353	4	US-09-731-030A-16
3	1772.5	95.9	354	3	US-09-325-897-2
4	1772.5	95.9	354	4	US-09-837-726-2
5	995	53.8	213	3	US-08-997-803-15
6	948.5	51.3	364	4	US-09-169-205D-20
7	948.5	51.3	364	4	US-09-731-030A-15
8	946.5	51.2	364	3	US-08-763-938-2
9	944.5	51.1	364	5	PCT-US96-10618-2
10	932.5	50.5	393	5	PCT-US96-10618-3
11	853.5	46.2	351	3	US-08-861-747-2
12	849.5	46.0	382	4	US-09-169-205D-23
13	843.5	45.6	351	3	US-08-789-982-2
14	843.5	45.6	352	4	US-09-582-200A-13
15	578.5	31.3	393	2	US-08-467-948A-4
16	578.5	31.3	393	3	US-08-467-947A-4
17	546	29.5	382	4	US-09-542-733-2
18	546	29.5	382	4	US-09-169-205D-21
19	541	29.3	383	1	US-08-196-989B-4
20	541	29.3	383	2	US-08-760-936-4
21	541	29.3	383	4	US-09-225-024-4
22	537	29.1	378	3	US-09-082-088-2
23	537	29.1	378	4	US-09-546-117-2
24	537	29.1	378	4	US-09-169-205D-22
25	537	29.1	378	4	US-09-731-030A-18
26	533.5	28.9	381	2	US-08-845-566-3
27	533.5	28.9	381	2	US-08-467-948A-28

28	533.5	28.9	381	3	US-08-852-824-18	Sequence 18, Appl
29	533.5	28.9	381	3	US-08-467-947A-28	Sequence 28, Appl
30	533.5	28.9	381	4	US-09-731-030A-17	Sequence 17, Appl
31	533.5	28.9	381	5	PCT-US96-10618-4	Sequence 4, Appl
32	532	28.8	382	4	US-09-262-477-2	Sequence 2, Appl
33	509.5	27.6	334	1	US-08-118-270-73	Sequence 73, Appl
34	509.5	27.6	334	5	PCT-US93-08528-73	Sequence 73, Appl
35	499	27.0	352	1	US-08-196-989B-2	Sequence 2, Appl
36	499	27.0	352	2	US-09-582-200A-11	Sequence 2, Appl
37	499	27.0	352	4	US-09-582-200A-11	Sequence 11, Appl
38	499	27.0	352	4	US-09-169-205D-24	Sequence 24, Appl
39	499	27.0	352	4	US-09-225-024-2	Sequence 2, Appl
40	474.5	25.7	353	4	US-09-582-200A-4	Sequence 4, Appl
41	474.5	25.7	353	4	US-09-582-200A-6	Sequence 6, Appl
42	474.5	25.7	353	4	US-09-582-200A-12	Sequence 12, Appl
43	474.5	25.7	353	4	US-09-731-030A-19	Sequence 19, Appl
44	473.5	25.6	353	4	US-09-582-200A-2	Sequence 2, Appl
45	473.5	25.6	353	4	US-09-582-200A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-997-803-14
Sequence 14, Application US/08997803
Patent No. 6057126

GENERAL INFORMATION:

APPLICANT: CHUN, Jerald J.M.
APPLICANT: GUPTA, Ashwani
APPLICANT: MUNROE, Donald G.
APPLICANT: VYAS, Tejal B.
TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Nixalco, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street, N.W., Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,803
FILING DATE: 24-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wong, King L.
REGISTRATION NUMBER: 37,500
REFERENCE/DOCKET NUMBER: P8074-7020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-803-14

Query Match 100.0%; Score 1848; DB 3; Length 353;
Best Local Similarity 100.0%; Pred.No. 3.5e-151;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNECHYDKHMDFFYRNSNTDVTGKLVIVLCVGFPCFFIFPSNSLYIAVYIKRK 60
DB 1 MNECHYDKHMDFFYRNSNTDVTGKLVIVLCVGFPCFFIFPSNSLYIAVYIKRK 60

QY 61 FHPEFYLLANLAADFPAGIAYVFLMNTGPVSKITLVNRMFLROGLDLSLSTASLTNL 120
| | | | |
Db 61 FHPEFYLLANLAADFPAGIAYVFLMNTGPVSKITLVNRMFLROGLDLSLSTASLTNL 120
QY 121 LVIAVERHMSIMRVRVSNLTGKRVTLILLVMAIAIFMGAVPTLGNCLCNISACSSLA 180
| | | | |
Db 121 LVIAVERHMSIMRVRVSNLTGKRVTLILLVMAIAIFMGAVPTLGNCLCNISACSSLA 180
QY 181 PIYSRSYLVTWVSNLMAFLIMVVYLRIVYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
| | | | |
Db 181 PIYSRSYLVTWVSNLMAFLIMVVYLRIVYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
QY 241 VMTVLGAFVVCWPTGLVVLPLDGLNCRCQGVQVHKRMFLALLALNSVNPPIYSYKDEDM 300
| | | | |
Db 241 VMTVLGAFVVCWPTGLVVLPLDGLNCRCQGVQVHKRMFLALLALNSVNPPIYSYKDEDM 300
QY 301 YGTAKKMICCFSEQENPERRPSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
| | | | |
Db 301 YGTAKKMICCFSEQENPERRPSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353

SOUT 2

US-09-731-030A-16
: Sequence 16, Application US/09731030A
: Patent No. 6566096
: GENERAL INFORMATION:
: APPLICANT: MUNKOE, Donald G
: APPLICANT: GUPTA, Ashwani K.
: APPLICANT: ZASTANY, Roman L.
: TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
: FILE REFERENCE: 8074-0015
: CURRENT APPLICATION NUMBER: US/09/731.030A
: PRIOR FILING DATE: 1998-12-29
: PRIOR APPLICATION NUMBER: 60/070,184
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 16
: LENGTH: 353
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG
US-09-731-030A-16

Query Match 99.5%; Score 1838; DB 4; Length 353;
Best Local Similarity 99.7%; Pred. No. 2.5e-150;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 FHPEFYLLANLAADFPAGIAYVFLMNTGPVSKITLVNRMFLROGLDLSLSTASLTNL 120
| | | | |
Db 61 FHPEFYLLANLAADFPAGIAYVFLMNTGPVSKITLVNRMFLROGLDLSLSTASLTNL 120
QY 121 LVIAVERHMSIMRVRVSNLTGKRVTLILLVMAIAIFMGAVPTLGNCLCNISACSSLA 180
| | | | |
Db 121 LVIAVERHMSIMRVRVSNLTGKRVTLILLVMAIAIFMGAVPTLGNCLCNISACSSLA 180
QY 181 PIYSRSYLVTWVSNLMAFLIMVVYLRIVYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
| | | | |
Db 181 PIYSRSYLVTWVSNLMAFLIMVVYLRIVYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
QY 241 VMTVLGAFVVCWPTGLVVLPLDGLNCRCQGVQVHKRMFLALLALNSVNPPIYSYKDEDM 300
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Db 241 VMTVLGAFVVCWPTGLVVLPLDGLNCRCQGVQVHKRMFLALLALNSVNPPIYSYKDEDM 300
QY 301 YGTAKKMICCFSEQENPERRPSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
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Db 301 YGTAKKMICCFSEQENPERRPSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353

RESULT 3

US-09-325-897-2
: Sequence 2, Application US/09325897
: Patent No. 6242572
: GENERAL INFORMATION:
: APPLICANT: Ping Tsui
: APPLICANT: Catherine E. Ellis
: APPLICANT: Ganesh M. Sathe
: APPLICANT: Stephanie Van Horn
: APPLICANT: Robert S. Ames
: APPLICANT: James J. Foley
: APPLICANT: Laura R. Fitzgerald
: APPLICANT: Harry M. Sarau
: TITLE OF INVENTION: HUMAN G PROTEIN COUPLED RECEPTOR
: FILE REFERENCE: GH70014-2
: CURRENT APPLICATION NUMBER: US/09/325.897
: EARLIER FILING DATE: 1999-06-04
: EARLIER FILING DATE: 1998-12-18
: EARLIER FILING DATE: 1998-12-18
: EARLIER FILING DATE: 08/992,031
: EARLIER FILING DATE: 1997-12-17
: EARLIER FILING DATE: 1997-05-13
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 354
: TYPE: PRT
: ORGANISM: Human
US-09-325-897-2

Query Match 95.9%; Score 1772.5; DB 3; Length 354;
Best Local Similarity 96.0%; Pred. No. 1.1e-144;
Matches 340; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 MNECHYKHMDFEYFNRSNTDTVDWGTGKLVIVLCVGFECLETFPSNSLYIAVIRNRK 60
| | | | |
Db 1 MNECHYKHMDFEYFNRSNTDTVDWGTGKLVIVLCVGFECLETFPSNSLYIAVIRNRK 60
QY 61 FHPEFYLLANLAADFPAGIAYVFLMNTGPVSKITLVNRMFLROGLDLSLSTASLTNL 120
| | | | |
Db 61 FHPEFYLLANLAADFPAGIAYVFLMNTGPVSKITLVNRMFLROGLDLSLSTASLTNL 120
QY 121 LVIAVERHMSIMRVRVSNLTGKRVTLILLVMAIAIFMGAVPTLGNCLCNISACSSLA 180
| | | | |
Db 121 LVIAVERHMSIMRVRVSNLTGKRVTLILLVMAIAIFMGAVPTLGNCLCNISACSSLA 180
QY 181 PIYSRSYLVTWVSNLMAFLIMVVYLRIVYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
| | | | |
Db 181 PIYSRSYLVTWVSNLMAFLIMVVYLRIVYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
QY 241 VMTVLGAFVVCWPTGLVVLPLDGLNCRCQGVQVHKRMFLALLALNSVNPPIYSYKDEDM 300
| | | | |
Db 241 VMTVLGAFVVCWPTGLVVLPLDGLNCRCQGVQVHKRMFLALLALNSVNPPIYSYKDEDM 300
QY 301 YGTAKKMICCFSEQENPERRPSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
| | | | |
Db 301 YGTAKKMICCFSEQENPERRPSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 354

RESULT 4

US-09-837-726-2
: Sequence 2, Application US/09837726
: Patent No. 6344342

: GENERAL INFORMATION:
: APPLICANT: Tsui, Ping
: APPLICANT: Ellis, Catherine E.
: APPLICANT: Sathe, Ganesh M.
: APPLICANT: Van Horn, Stephanie
: APPLICANT: Ames, Robert A.
: APPLICANT: Foley, James J.

APPLICANT: Fitzgerald, Laura
 APPLICANT: Sarau, Henry M.
 TITLE OF INVENTION: HUMAN G PROTEIN COUPLED RECEPTOR
 FILE REFERENCE: GH-70014-D3
 CURRENT APPLICATION NUMBER: US/09/837,726
 PRIOR FILING DATE: 2001-04-18
 PRIOR APPLICATION NUMBER: 60/046,366
 PRIOR FILING DATE: 1997-05-13
 PRIOR APPLICATION NUMBER: 08/992,031
 PRIOR FILING DATE: 1997-12-17
 PRIOR APPLICATION NUMBER: 09/215,072
 PRIOR FILING DATE: 1998-12-18
 PRIOR APPLICATION NUMBER: 09/325,897
 PRIOR FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: FastSeq for Windows version 3.0
 SEQ ID NO 2
 LENGTH: 354
 TYPE: PRT
 ORGANISM: HOMO SAPIENS
 S-09-837-726-2

Query Match 95.9%; Score 1772.5; DB 4; Length 354;
 Best Local Similarity 96.0%; Pred. No. 1.1e-144;
 Matches 340; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 MNECHYDHDHDFEYKRSNTDVTGTRIVYLCVGFECLEFFFSNLSVIAAVIKNK 60
 DB 1 MNECHYDHDHDFEYKRSNTDVTGTRIVYLCVGFECLEFFFSNLSVIAAVIKNK 60
 QY 61 FHPEPYLLANLAADFFAGIAYVFLMNTGVSSTLVNRMFLROGLDSSITASLTNL 120
 DB 61 FHPEPYLLANLAADFFAGIAYVFLMNTGVSSTLVNRMFLROGLDSSITASLTNL 120
 QY 121 LVIAERHMSIMRBMVHNSLTKKRYTLILLVMAIAIFMGAVPTLGWNCICNISCSLA 180
 DB 121 LVIAERHMSIMRBMVHNSLTKKRYTLILLVMAIAIFMGAVPTLGWNCICNISCSLA 180
 QY 181 PIYSRSYLVFWTYSNLMFLIMVYVYLRIYVYVKKRTVNLSPHTSGSISRRTPKMKMT 240
 DB 181 PIYSRSYLVFWTYSNLMFLIMVYVYLRIYVYVKKRTVNLSPHTSGSISRRTPKMKMT 240
 QY 241 VWTVLGAFFVWCTPGLVYVLPDGLNCRQCGVQVHKRWFLLLALLNSVNPPIYSKDEDM 300
 DB 241 VWTVLGAFFVWCTPGLVYVLPDGLNCRQCGVQVHKRWFLLLALLNSVNPPIYSKDEDM 300
 QY 301 YGTAKMKICCFSGE-NPERRPRISYLSRSDTSQYIEDSISGAVCNKSTS 353
 DB 301 YGTAKMKICCFSGE-NPERRPRISYLSRSDTSQYIEDSISGAVCNKSTS 353
 QY 301 YSTMKMKICCFSGE-NPERRPRISYLSRSDTSQYIEDSISGAVCNKSTS 354
 DB 301 YSTMKMKICCFSGE-NPERRPRISYLSRSDTSQYIEDSISGAVCNKSTS 354

RESULT 5
 US-08-997-803-15
 Sequence 15, Application US/08997803
 Patent No. 6057126

GENERAL INFORMATION:
 APPLICANT: CHUN, Jerald J. M.
 APPLICANT: GUPTA, Ashwani
 APPLICANT: MUNROE, Donald G.
 APPLICANT: VITAS, Tejal B.
 TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
 STREET: 655 Fifteenth Street, N.W., Suite 330
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-5701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/997,803
 FILING DATE: 24-DEC-1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Wong, King L.
 REGISTRATION NUMBER: 37,500
 REFERENCE/DOCKET NUMBER: P8074-7020
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 638-5000
 TELEFAX: (202) 638-4810
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 213 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-997-803-15

Query Match 53.8%; Score 995; DB 3; Length 213;
 Best Local Similarity 92.7%; Pred. No. 3.6e-78;
 Matches 190; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 89 NTGPVSKITLVNRWFLROGLDSSITASLTNLVIAERHMSIMRBMVHNSLTKKRYTL 148
 DB 1 NTGPVSKITLVNRWFLROGLDSSITASLTNLVIAERHMSIMRBMVHNSLTKKRYTL 148
 QY 149 ILLVMAIAIFMGAVPTLGWNCICNISCSLAPISRSYLVFWTYSNLMFLIMVYVYR 208
 DB 149 ILLVMAIAIFMGAVPTLGWNCICNISCSLAPISRSYLVFWTYSNLMFLIMVYVYR 208
 QY 209 IYVYVYKRTVNLSPHTSGSISRRTPKMKMTVWTLGAFVWCTPGLVYVLPDGLNCRQ 268
 DB 209 IYVYVYKRTVNLSPHTSGSISRRTPKMKMTVWTLGAFVWCTPGLVYVLPDGLNCRQ 268
 QY 269 CGVOHVRWFLLLALLNSVNPPIY 293
 DB 269 CGVOHVRWFLLLALLNSVNPPIY 293
 QY 181 CNVQHVXKWFLLALLNSVNPPIY 205
 DB 181 CNVQHVXKWFLLALLNSVNPPIY 205

RESULT 6
 US-09-169-205D-20
 Sequence 20, Application US/09169205D
 Patent No. 6485922

GENERAL INFORMATION:
 APPLICANT: Erikson, James
 APPLICANT: Goddard, J. Graham
 APPLICANT: Kieffer, Michael
 TITLE OF INVENTION: METHODS FOR DETECTING COMPOUNDS WHICH MODULATE THE
 TITLE OF INVENTION: ACTIVITY OF AN LPA RECEPTOR
 FILE REFERENCE: 252/004
 CURRENT APPLICATION NUMBER: US/09/169,205D
 CURRENT FILING DATE: 1998-10-09
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 20
 LENGTH: 364
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-169-205D-20

Query Match 51.3%; Score 948.5; DB 4; Length 364;
 Best Local Similarity 51.6%; Pred. No. 6.3e-74;
 Matches 175; Conservative 76; Mismatches 75; Indels 13; Gaps 5;

QY 1 MNECHYDHDHDFEYKRSNTDVTGTRIVYLCVGFECLEFFFSNLSVIAAVIK 57
 DB 1 MNECHYDHDHDFEYKRSNTDVTGTRIVYLCVGFECLEFFFSNLSVIAAVIK 57
 QY 19 MNECHYDHDHDFEYKRSNTDVTGTRIVYLCVGFECLEFFFSNLSVIAAVIK 76
 DB 19 MNECHYDHDHDFEYKRSNTDVTGTRIVYLCVGFECLEFFFSNLSVIAAVIK 76
 QY 58 NKEHPEPYLLANLAADFFAGIAYVFLMNTGVSSTLVNRMFLROGLDSSITASLTNL 117
 DB 58 NKEHPEPYLLANLAADFFAGIAYVFLMNTGVSSTLVNRMFLROGLDSSITASLTNL 117

Db 77 NRHFPIYIYMANLAADFFAGIAYFLMNTGENTRLVSTWLNROGLIDSLASV 136
 QY 118 TNLVIAVERMSIMRMRHSNLTAKRVTLILVMAIAIPMGAVPTLGNCLNISACS 177
 Db 137 ANLAIAIERHTIRMQLTMRNRVRYVIVYIMTAIYMGAIIPSGMNCIDIEACS 196
 QY 178 SLATYRSYLVETVSNLMAFLIMVYVLYLIIYVAKKTVLSPHISGTSRRRTPKL 237
 Db 197 NMAPLVSDSYLVAFIYFRLQHTMRNRVRYVIVYIMTAIYMGAIIPSGMNCIDIEACS 256
 QY 238 MKTYMTVLGAFVVCWPTGLVVLPLDGLNCRQGVQVHVRKRWFLTLALNSVNPPIIYSYKD 297
 Db 257 LKTYVIVYIGAFIICWPTGLVLLLD-VCCPQCDVLAYEKFFLLAEFNSANPPIIYSYRD 315
 QY 298 EDATGTMKMKICFSGQENP-----ERRPSRIPSTVLS 329
 Db 316 KEMSATFROIICCORSENPPTGTEGSDRSASLSLHNTILA 354

RESULT 7

-09-731-030A-15
 Sequence 15, Application US/09731030A
 Patent No. 6566096
 GENERAL INFORMATION:
 APPLICANT: MUNROE, Donald G.
 APPLICANT: GUPTA, Ashwani K.
 APPLICANT: ZASTAWNY, Roman L.
 TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
 FILE REFERENCE: 8074-0015
 CURRENT APPLICATION NUMBER: US/09/731,030A
 PRIOR FILING DATE: 1998-12-28
 PRIOR APPLICATION NUMBER: 60/070,184
 PRIOR FILING DATE: 1997-12-30
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 15
 LENGTH: 364
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG
 US-09-731-030A-15

Query Match 51.3% Score 948.5; DB 4; Length 364;
 Best Local Similarity 51.6% Pred. No. 6.3e-74;
 Matches 175; Conservative 76; Mismatches 75; Indels 13; Gaps 5;
 QY 1 MNE--CHYDKHMOEFYRNSNTDVTDDW-TGFKLYIVCYGTFECLTFEFSSTVIAVIR 57
 Db 19 MNEQCCYTNESIAFYRNSGKHLATEMNTVSKLVGL--GITVCIFIMLANLWVAIVY 76
 QY 58 NRKHFPEYIYLANLAADFFAGIAYFLMNTGVSCTLVNRMFLROGLDLSLSTASL 117
 Db 77 NRHFPIYIYMANLAADFFAGIAYFLMNTGPNTRLVSTWLNROGLIDSLASV 136
 QY 118 TNLVIAVERMSIMRMRHSNLTAKRVTLILVMAIAIPMGAVPTLGNCLNISACS 177
 Db 137 ANLAIAIERHTIRMQLTMRNRVRYVIVYIMTAIYMGAIIPSGMNCIDIEACS 196
 QY 178 SLATYRSYLVETVSNLMAFLIMVYVLYLIIYVAKKTVLSPHISGTSRRRTPKL 237
 Db 197 NMAPLVSDSYLVAFIYFRLQHTMRNRVRYVIVYIMTAIYMGAIIPSGMNCIDIEACS 256
 QY 238 MKTYMTVLGAFVVCWPTGLVVLPLDGLNCRQGVQVHVRKRWFLTLALNSVNPPIIYSYKD 297
 Db 257 LKTYVIVYIGAFIICWPTGLVLLLD-VCCPQCDVLAYEKFFLLAEFNSANPPIIYSYRD 315
 QY 298 EDATGTMKMKICFSGQENP-----ERRPSRIPSTVLS 329
 Db 316 KEMSATFROIICCORSENPPTGTEGSDRSASLSLHNTILA 354

RESULT 8

US-08-763-938-2
 Sequence 2, Application US/08763938
 Patent No. 6140060
 GENERAL INFORMATION:
 APPLICANT: CHUN, Jeroald J.M.
 APPLICANT: HECHT, Jonathan H.
 TITLE OF INVENTION: CLONED LYSOPHOSPHATIDIC ACID
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nikaido, Matmelsstein, Murray and Oram LLP
 STREET: 655 15th Street, N.W., Suite 350 - G St. Lobby
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-5701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/763,938
 FILING DATE: 12-DEC-1996
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: JAHNS, Kristina M.
 REGISTRATION NUMBER: 41,092
 REFERENCE/DOCKET NUMBER: P8074-6018
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 638-5000
 TELEFAX: (202) 638-4810
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 364 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-763-938-2

Query Match 51.2% Score 946.5; DB 3; Length 364;
 Best Local Similarity 51.9% Pred. No. 9.4e-74;
 Matches 176; Conservative 75; Mismatches 75; Indels 13; Gaps 5;
 QY 1 MNE--CHYDKHMOEFYRNSNTDVTDDW-TGFKLYIVCYGTFECLTFEFSSTVIAVIR 57
 Db 19 MNEQCCYTNESIAFYRNSGKHLATEMNTVSKLVGL--GITVCIFIMLANLWVAIVY 76
 QY 58 NRKHFPEYIYLANLAADFFAGIAYFLMNTGVSCTLVNRMFLROGLDLSLSTASL 117
 Db 77 NRHFPIYIYMANLAADFFAGIAYFLMNTGPNTRLVSTWLNROGLIDSLASV 136
 QY 118 TNLVIAVERMSIMRMRHSNLTAKRVTLILVMAIAIPMGAVPTLGNCLNISACS 177
 Db 137 ANLAIAIERHTIRMQLTMRNRVRYVIVYIMTAIYMGAIIPSGMNCIDIEACS 196
 QY 178 SLATYRSYLVETVSNLMAFLIMVYVLYLIIYVAKKTVLSPHISGTSRRRTPKL 237
 Db 197 NMAPLVSDSYLVAFIYFRLQHTMRNRVRYVIVYIMTAIYMGAIIPSGMNCIDIEACS 256
 QY 238 MKTYMTVLGAFVVCWPTGLVVLPLDGLNCRQGVQVHVRKRWFLTLALNSVNPPIIYSYKD 297
 Db 257 LKTYVIVYIGAFIICWPTGLVLLLD-VCCPQCDVLAYEKFFLLAEFNSANPPIIYSYRD 315
 QY 298 EDATGTMKMKICFSGQENP-----ERRPSRIPSTVLS 329
 Db 316 KEMSATFROIICCORSENPPTGTEGSDRSASLSLHNTILA 354

RESULT 9

PCT-US96-10618-2
 Sequence 2, Application PC/TUS9610618


```

; TITLE OF INVENTION: cDNA CLONE HB8CH90 THAT ENCODES
; TITLE OF INVENTION: A NOVEL 7- TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,982
; FILING DATE: 28-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: AIG50050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-789-982-2

Query Match      45.6%; Score 843.5; DB 3; Length 351;
Best Local Similarity 50.3%; Pred. No. 6.3e-65;
Matches 156; Conservative 60; Mismatches 93; Indels 1; Gaps 1;

OY 1 MNECHYKHMDFEYRNSNTDVTGTRKLVIVLCVGFECLEFFESNSLYIAAVIKNRK 60
DB 4 MGOCYVNETIGFYNNNGKELSSHR-PRDYVVALGLVSVLYLTNLNLTAAIASNR 62
OY 61 FHFPPYYLLANLAADFFAGIAYVFLMNTGVSRTLVNRFLLROGLDSSLTASLNL 120
DB 63 FHQPTYYLLGNLAADLFAGVAYLFLMFTGRTALSLGFWFLROGLDTSLTASVATL 122
OY 121 LVIAVERHMSIRMRHNSLTKKRVTLILLWMAIFMGAVPTGWNCLCNISACSSLA 180
DB 123 LAIAVERHRSVAVALHSLRPRGRVYMLIVGWMAALGCLIPASHMCLCALDRCSRA 182
OY 181 PYSRSYLVFWTNSIMAEFLIMVYVYLRITYYVKKRTNVLSPHTSGSISRRTPKIMKT 240
DB 183 PLTSRSYLAVALMSLVFLMLVAVYTRIFVYRRVQMAHVSCHPRYRTTSLVKT 242
OY 241 VMTVIGAFVVCWTPGVLVPLDGLNCRGCGVQVHKRMFLALLNSVNPPIYSKDEDM 300
DB 243 VIIIGAFVVCWTPGQVYLLDGLGCSGCVLAVERKYLFLLEANSLSVAAYVSCRDADM 302
OY 301 YGTMKMIC 310
DB 303 RTFRRLCC 312

RESULT 14
US-09-582-200A-13
; Sequence 13, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:

```

```

; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejpal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human ED6-6 receptor
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (352)..(352)
; OTHER INFORMATION: "Xaa" represents any amino acid
; US-09-582-200A-13

Query Match      45.6%; Score 843.5; DB 4; Length 352;
Best Local Similarity 50.3%; Pred. No. 6.3e-65;
Matches 156; Conservative 60; Mismatches 93; Indels 1; Gaps 1;

OY 1 MNECHYKHMDFEYRNSNTDVTGTRKLVIVLCVGFECLEFFESNSLYIAAVIKNRK 60
DB 4 MGOCYVNETIGFYNNNGKELSSHR-PRDYVVALGLVSVLYLTNLNLTAAIASNR 62
OY 61 FHFPPYYLLANLAADFFAGIAYVFLMNTGVSRTLVNRFLLROGLDSSLTASLNL 120
DB 63 FHQPTYYLLGNLAADLFAGVAYLFLMFTGRTALSLGFWFLROGLDTSLTASVATL 122
OY 121 LVIAVERHMSIRMRHNSLTKKRVTLILLWMAIFMGAVPTGWNCLCNISACSSLA 180
DB 123 LAIAVERHRSVAVALHSLRPRGRVYMLIVGWMAALGCLIPASHMCLCALDRCSRA 182
OY 181 PYSRSYLVFWTNSIMAEFLIMVYVYLRITYYVKKRTNVLSPHTSGSISRRTPKIMKT 240
DB 183 PLTSRSYLAVALMSLVFLMLVAVYTRIFVYRRVQMAHVSCHPRYRTTSLVKT 242
OY 241 VMTVIGAFVVCWTPGVLVPLDGLNCRGCGVQVHKRMFLALLNSVNPPIYSKDEDM 300
DB 243 VIIIGAFVVCWTPGQVYLLDGLGCSGCVLAVERKYLFLLEANSLSVAAYVSCRDADM 302
OY 301 YGTMKMIC 310
DB 303 RTFRRLCC 312

RESULT 15
US-08-467-948A-4
; Sequence 4, Application US/08467948A
; Patent No. 598164
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BOLT, CAROL J.
; APPLICANT: SOTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.

```

TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
 FILE OF INVENTION: Coupled Receptor GPR2
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.,
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,948A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEEFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 393 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 JS-08-467-948A-4

Query Match	31.3%	Score 578.5	DB 2	Length 393
Best Local Similarity	44.5%	Pred. No. 4.1e-42		
Matches 117; Conservative	47	Mismatches 88	Indels 11	Gaps 1

QY	68	LLANLAAADPAGIAYVPELMEFTGVSTLTIVNRMFLRGGLDSSLTALTLNLTAVAR	127
		: : : : : : : : : : : : : : : : : : :	
Db	72	LRAULSAAADLRGRCLPPEVPHPCRTARLTSEGFELRGGLDNTINTASVATLLTAIVER	131
		: : : : : : : : : : : : : : : : : : :	
QY	128	HMSIMRMKRVHNSLTKRKVTLILLVMAIAIFMGAVPTLGWNLCSACSSLAPIYSRSY	187
		: : : : : : : : : : : : : : : : : : :	
Db	132	HRSYAAVAQJHSLRPLPGRGVYVMLIVGVMAALGGLPAHSHWICLCALDRSSRAAPLLSRSY	191
		: : : : : : : : : : : : : : : : : : :	
QY	188	LVPEFTVNSLMAFLIMVYVYLRIRYVYVKRKNTLSPTSSISIRRRPMLMTVMYVLGA	247
		: : : : : : : : : : : : : : : : : : :	
Db	192	LAVMALSTLFLMLVAAYYTRITFEFVVRKRVQMAEHSVCHPRYRETTLSLVKTVYLLIDA	251
		: : : : : : : : : : : : : : : : : : :	
QY	248	FVVCWMTPEGLVYLPLDGLNCROQGVQVHYVRKMFLLALLNSVNPPIIYSYDEYDEMGTKMK	307
		: : : : : : : : : : : : : : : : : : :	
Db	252	FVVCWMTPEQVYVLLDGLGCESCQNVYALEREYFLLLAEPSTLVNAAYVSCDAEMKRRFRRL	311
		: : : : : : : : : : : : : : : : : : :	
QY	308	ICCFSGQENPERPRRIPESTVLSR	330
		: : : : : : : : : : : : : : : : : : :	
Db	312	LLL-----RVPPVHR	323

Search completed: August 18, 2003, 15:19:56
Job time : 31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2003, 15:12:14 ; Search time 57 Seconds

(without alignments)
811.301 Million cell updates/sec

Title: US-09-581-252-14

Perfect score: 1848
Sequence: 1 MNECHYDKHMDFFYNRSNTD.....GSQYIEDISOGAVCNKSTS 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Minimum number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCY_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1838	99.5	353	9 US-09-842-316-4	Sequence 4, Appl1
2	1838	99.5	353	10 US-09-731-030A-16	Sequence 16, Appl1
3	1838	99.5	353	10 US-09-971-228-11	Sequence 11, Appl1
4	1838	99.5	353	11 US-09-811-838-6	Sequence 6, Appl1
5	1838	99.5	353	11 US-09-904-099-35	Sequence 35, Appl1
6	1838	99.5	353	12 US-09-953-686-6	Sequence 6, Appl1
7	1838	99.5	353	12 US-10-037-616-25	Sequence 25, Appl1
8	1838	99.5	353	15 US-10-097-340-338	Sequence 338, App
9	1838	99.5	353	15 US-10-225-567A-553	Sequence 353, App
10	1838	99.5	353	16 US-10-228-762-2	Sequence 2, Appl1
11	1692.5	91.6	354	9 US-09-879-225-2	Sequence 2, Appl1
12	1014.5	54.9	220	15 US-10-073-885-80	Sequence 80, Appl1
13	948.5	51.3	364	9 US-09-842-316-3	Sequence 3, Appl1
14	948.5	51.3	364	10 US-09-731-030A-15	Sequence 15, Appl1
15	948.5	51.3	364	10 US-09-971-228-6	Sequence 6, Appl1

16	948.5	51.3	364	11 US-09-811-838-2	Sequence 2, Appl1
17	948.5	51.3	364	11 US-09-904-099-30	Sequence 30, Appl1
18	948.5	51.3	364	12 US-09-953-686-2	Sequence 2, Appl1
19	948.5	51.3	364	14 US-10-037-616-20	Sequence 20, Appl1
20	948.5	51.3	364	15 US-10-225-567A-152	Sequence 152, App
21	948.5	51.3	364	16 US-10-228-762-15	Sequence 15, Appl1
22	849.5	46.0	348	9 US-09-903-799-2	Sequence 2, Appl1
23	849.5	46.0	382	9 US-09-842-316-5	Sequence 5, Appl1
24	849.5	46.0	382	11 US-09-904-099-32	Sequence 32, Appl1
25	849.5	46.0	382	16 US-10-228-762-16	Sequence 16, Appl1
26	843.5	45.6	351	10 US-09-971-228-8	Sequence 8, Appl1
27	843.5	45.6	351	11 US-09-811-838-4	Sequence 4, Appl1
28	843.5	45.6	351	11 US-09-904-099-31	Sequence 31, Appl1
29	843.5	45.6	351	12 US-09-953-686-4	Sequence 4, Appl1
30	843.5	45.6	351	14 US-10-037-616-22	Sequence 22, Appl1
31	843.5	45.6	351	15 US-10-084-507B-23	Sequence 23, Appl1
32	843.5	45.6	351	15 US-10-225-567A-350	Sequence 350, App
33	578.5	31.3	393	15 US-10-024-494-4	Sequence 4, Appl1
34	547	29.6	384	9 US-09-904-099-4	Sequence 4, Appl1
35	546	29.5	382	9 US-09-969-711-2	Sequence 4, Appl1
36	546	29.5	384	11 US-09-904-099-5	Sequence 5, Appl1
37	541.5	29.3	391	11 US-09-904-099-3	Sequence 3, Appl1
38	537	29.1	378	9 US-09-842-316-7	Sequence 7, Appl1
39	537	29.1	378	10 US-09-731-030A-18	Sequence 18, Appl1
40	537	29.1	378	10 US-09-971-228-7	Sequence 7, Appl1
41	537	29.1	378	11 US-09-904-099-2	Sequence 21, Appl1
42	537	29.1	378	14 US-10-037-616-21	Sequence 21, Appl1
43	537	29.1	378	15 US-10-225-567A-239	Sequence 239, App
44	537	29.1	378	16 US-10-228-762-18	Sequence 18, Appl1
45	533.5	28.9	381	9 US-09-827-937A-18	Sequence 18, Appl1

ALIGNMENTS

RESULT 1
US-09-842-316-4
; Sequence 4, Application US/09842316
; Patent No. US20020099191A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENSIS, Eva
; APPLICANT: CASSENHUBER, Johann
; TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE
; FILE REFERENCE: 38005-147
; CURRENT APPLICATION NUMBER: US/09/842,316
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: EP 116589.3
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: EP 108858.2
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-842-316-4

Query Match	Score 1838:	DB 9:	Length 353:
Best Local Similarity	99.7%:	Pred. No. 4e-170:	1: Indels 0: Gaps 0:
Matches 352:	Conservative	0: Mismatches	1: Indels 0: Gaps 0:

QY 1 MNECHYDKHMDFFYNRSNTDVTGTLVIVLCGPFCLFFFSNLSVIAAYIKNK 60
DB 1 MNECHYDKHMDFFYNRSNTDVTGTLVIVLCGPFCLFFFSNLSVIAAYIKNK 60
QY 61 FHEPPYLIANLAADDFAGIAYVFLMFTGVSSTLVVNRFLRQGLDSSLTASLTNL 120
DB 61 FHEPPYLIANLAADDFAGIAYVFLMFTGVSSTLVVNRFLRQGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMRKHSHSLTKRKRYTLILLVMAIAIFGAVPTLGWNCISACSSIA 180
DB 121 LVIAVERHMSIMRKHSHSLTKRKRYTLILLVMAIAIFGAVPTLGWNCISACSSIA 180

; CURRENT APPLICATION NUMBER: US/09/811.838
 ; CURRENT FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 60/1290,370
 ; PRIOR FILING DATE: 2000-03-17
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 353
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-811-838-6

Query Match 99.5%; Score 1838; DB 11; Length 353;
 Best Local Similarity 99.7%; Pred. No. 4e-170;
 Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNECHYDKHMDFFYRNSMTDVTGDKLYIVLCVGFECFLFFFSNSLYIAAIVKRRK 60
 DB 1 MNECHYDKHMDFFYRNSMTDVTGDKLYIVLCVGFECFLFFFSNSLYIAAIVKRRK 60
 QY 61 FHFPYYLLANLAADFFAGIAYVFLMNTGVSRTLVNRMFLROGLDSSLTASLTNL 120
 DB 61 FHFPYYLLANLAADFFAGIAYVFLMNTGVSRTLVNRMFLROGLDSSLTASLTNL 120
 QY 121 LVIAVERHMSIMRMVHNSLTKRRVTLILVMAIAIFMGAVPTLGMNCLNISACSSIA 180
 DB 121 LVIAVERHMSIMRMVHNSLTKRRVTLILVMAIAIFMGAVPTLGMNCLNISACSSIA 180
 QY 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRITYYVKKRTNVLSPHSGSISRRTPKMLKT 240
 DB 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRITYYVKKRTNVLSPHSGSISRRTPKMLKT 240
 QY 241 VMTVGAFCVWCPGLVYLPLDGLNCRQCGVQHVAKRMFLALLNSVYVNPITYSKDEDM 300
 DB 241 VMTVGAFCVWCPGLVYLPLDGLNCRQCGVQHVAKRMFLALLNSVYVNPITYSKDEDM 300
 QY 301 YGTMMKMICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISQAVCNKSTS 353
 DB 301 YGTMMKMICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISQAVCNKSTS 353

RESULT 5
 US-09-904-099-35
 ; Sequence 35, Application US/09904099
 ; Publication No. US20030119092A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shankar, Geetha
 ; APPLICANT: Munnung, Jason N
 ; APPLICANT: Spencer, Juliet V
 ; TITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: 10602-013-999
 ; CURRENT APPLICATION NUMBER: US/09/904,099
 ; CURRENT FILING DATE: 2001-07-11
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 35
 ; LENGTH: 353
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-904-099-35

Query Match 99.5%; Score 1838; DB 11; Length 353;
 Best Local Similarity 99.7%; Pred. No. 4e-170;
 Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNECHYDKHMDFFYRNSMTDVTGDKLYIVLCVGFECFLFFFSNSLYIAAIVKRRK 60
 DB 1 MNECHYDKHMDFFYRNSMTDVTGDKLYIVLCVGFECFLFFFSNSLYIAAIVKRRK 60
 QY 61 FHFPYYLLANLAADFFAGIAYVFLMNTGVSRTLVNRMFLROGLDSSLTASLTNL 120
 DB 61 FHFPYYLLANLAADFFAGIAYVFLMNTGVSRTLVNRMFLROGLDSSLTASLTNL 120

QY 121 LVIAVERHMSIMRMVHNSLTKRRVTLILVMAIAIFMGAVPTLGMNCLNISACSSIA 180
 DB 121 LVIAVERHMSIMRMVHNSLTKRRVTLILVMAIAIFMGAVPTLGMNCLNISACSSIA 180
 QY 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRITYYVKKRTNVLSPHSGSISRRTPKMLKT 240
 DB 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRITYYVKKRTNVLSPHSGSISRRTPKMLKT 240
 QY 241 VMTVGAFCVWCPGLVYLPLDGLNCRQCGVQHVAKRMFLALLNSVYVNPITYSKDEDM 300
 DB 241 VMTVGAFCVWCPGLVYLPLDGLNCRQCGVQHVAKRMFLALLNSVYVNPITYSKDEDM 300
 QY 301 YGTMMKMICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISQAVCNKSTS 353
 DB 301 YGTMMKMICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISQAVCNKSTS 353

RESULT 6
 US-09-953-686-6
 ; Sequence 6, Application US/09953686
 ; Publication No. US20030130237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Miller, Duane D.
 ; APPLICANT: Tigy1, Gabor
 ; APPLICANT: Dalton, James T.
 ; APPLICANT: Sardar, Vineet M.
 ; APPLICANT: Elrod, Don B.
 ; APPLICANT: Xu, Huijing
 ; APPLICANT: Baker, Daniel L.
 ; APPLICANT: Wang, Dean
 ; APPLICANT: Lillom, Karoly
 ; APPLICANT: Fischer, David J.
 ; APPLICANT: Virag, Tamas
 ; APPLICANT: Nusser, No. US20030130237A1a
 ; TITLE OF INVENTION: LRA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
 ; FILE REFERENCE: 20609/183
 ; CURRENT APPLICATION NUMBER: US/09/953,686
 ; CURRENT FILING DATE: 2002-05-21
 ; PRIOR APPLICATION NUMBER: 09/811,838
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 353
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-953-686-6

Query Match 99.5%; Score 1838; DB 12; Length 353;
 Best Local Similarity 99.7%; Pred. No. 4e-170;
 Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNECHYDKHMDFFYRNSMTDVTGDKLYIVLCVGFECFLFFFSNSLYIAAIVKRRK 60
 DB 1 MNECHYDKHMDFFYRNSMTDVTGDKLYIVLCVGFECFLFFFSNSLYIAAIVKRRK 60
 QY 61 FHFPYYLLANLAADFFAGIAYVFLMNTGVSRTLVNRMFLROGLDSSLTASLTNL 120
 DB 61 FHFPYYLLANLAADFFAGIAYVFLMNTGVSRTLVNRMFLROGLDSSLTASLTNL 120
 QY 121 LVIAVERHMSIMRMVHNSLTKRRVTLILVMAIAIFMGAVPTLGMNCLNISACSSIA 180
 DB 121 LVIAVERHMSIMRMVHNSLTKRRVTLILVMAIAIFMGAVPTLGMNCLNISACSSIA 180
 QY 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRITYYVKKRTNVLSPHSGSISRRTPKMLKT 240
 DB 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRITYYVKKRTNVLSPHSGSISRRTPKMLKT 240
 QY 241 VMTVGAFCVWCPGLVYLPLDGLNCRQCGVQHVAKRMFLALLNSVYVNPITYSKDEDM 300
 DB 241 VMTVGAFCVWCPGLVYLPLDGLNCRQCGVQHVAKRMFLALLNSVYVNPITYSKDEDM 300

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QY 301 YGTMKMICFSEQENPERRPSRIPSTVLSRSDGSGYIEDSISOGAVCNKSTS 353
Db 301 YGTMKMICFSEQENPERRPSRIPSTVLSRSDGSGYIEDSISOGAVCNKSTS 353

RESULT 7
US-10-037-616-25
; Sequence 25, Application US/10037616
; Publication No. US20020123148A1
; GENERAL INFORMATION:
; APPLICANT: English, Denis
; APPLICANT: Kovacs, Richard J.
; APPLICANT: Rizzo, Maria T.
; APPLICANT: Silva, Daniel T.
; TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic Use
; FILE REFERENCE: 7042-119
; CURRENT APPLICATION NUMBER: US/10/037,616
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/243,887
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 353
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-037-616-25

Query Match 99.5%; Score 1838; DB 14; Length 353;
Best Local Similarity 99.7%; Pred. No. 4e-170; Indels 0; Gaps 0;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MNECHYDKHMDFFYNSNTDTVDWGTGKLIYLCVGTFFCLIFFSNSLVIAVKNRK 60

QY 61 FHPEFYLLANLAAAFAGIAYVFLMNTGPKVSKITLVNRMFLROGLDSSSLASTLNL 120
Db 61 FHPEFYLLANLAAAFAGIAYVFLMNTGPKVSKITLVNRMFLROGLDSSSLASTLNL 120

QY 121 LVIAVERHMSIMRVRHSNLTKKRVTLILLVMAAIFMGAVPTLGNCLNISACSSLA 180
Db 121 LVIAVERHMSIMRVRHSNLTKKRVTLILLVMAAIFMGAVPTLGNCLNISACSSLA 180

QY 181 PIYSRSYLVFWYWSNLMAFILMVVYLRITYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
Db 181 PIYSRSYLVFWYWSNLMAFILMVVYLRITYVYKRTNVLSPHTSGSISRRTPMKLMKT 240

QY 241 VMTVLGAFVVCWTPGLVVLPLDGLNCRGCGVQHVKKRFFLLALLNSVYVNPITISYKDEDM 300
Db 241 VMTVLGAFVVCWTPGLVVLPLDGLNCRGCGVQHVKKRFFLLALLNSVYVNPITISYKDEDM 300

QY 301 YGTMKMICFSEQENPERRPSRIPSTVLSRSDGSGYIEDSISOGAVCNKSTS 353
Db 301 YGTMKMICFSEQENPERRPSRIPSTVLSRSDGSGYIEDSISOGAVCNKSTS 353

RESULT 8
US-10-097-340-338
; Sequence 338, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
```

```
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumel ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 338
; LENGTH: 353
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-097-340-338

Query Match 99.5%; Score 1838; DB 15; Length 353;
Best Local Similarity 99.7%; Pred. No. 4e-170; Indels 1; Gaps 0;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNECHYDKHMDFFYNSNTDTVDWGTGKLIYLCVGTFFCLIFFSNSLVIAVKNRK 60
Db 1 MNECHYDKHMDFFYNSNTDTVDWGTGKLIYLCVGTFFCLIFFSNSLVIAVKNRK 60

QY 61 FHPEFYLLANLAAAFAGIAYVFLMNTGPKVSKITLVNRMFLROGLDSSSLASTLNL 120
Db 61 FHPEFYLLANLAAAFAGIAYVFLMNTGPKVSKITLVNRMFLROGLDSSSLASTLNL 120

QY 121 LVIAVERHMSIMRVRHSNLTKKRVTLILLVMAAIFMGAVPTLGNCLNISACSSLA 180
Db 121 LVIAVERHMSIMRVRHSNLTKKRVTLILLVMAAIFMGAVPTLGNCLNISACSSLA 180

QY 181 PIYSRSYLVFWYWSNLMAFILMVVYLRITYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
Db 181 PIYSRSYLVFWYWSNLMAFILMVVYLRITYVYKRTNVLSPHTSGSISRRTPMKLMKT 240

QY 241 VMTVLGAFVVCWTPGLVVLPLDGLNCRGCGVQHVKKRFFLLALLNSVYVNPITISYKDEDM 300
Db 241 VMTVLGAFVVCWTPGLVVLPLDGLNCRGCGVQHVKKRFFLLALLNSVYVNPITISYKDEDM 300

QY 301 YGTMKMICFSEQENPERRPSRIPSTVLSRSDGSGYIEDSISOGAVCNKSTS 353
Db 301 YGTMKMICFSEQENPERRPSRIPSTVLSRSDGSGYIEDSISOGAVCNKSTS 353

RESULT 9
US-10-225-567A-553
; Sequence 553, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Butner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
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;; CURRENT FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 60/257,144
;; PRIOR FILING DATE: 2000-12-19
;; NUMBER OF SEQ ID NOS: 2292
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 553
;; LENGTH: 353
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-225-567A-553

Query Match 99.5%; Score 1838; DB 15; Length 353;
Best Local Similarity 99.7%; Pred. No. 4e-170;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MNECHYKHMDFNRSNTDVTVDWMTGKLVILCVGTFECLFIFSSLSVIAAYTKRK 60
QY 61 FHFFPYLLANLAADFFAGIAYVFLMNTGVSRTLTNNRMFLROGLDSSLTASLTNL 120
DB 61 FHFFPYLLANLAADFFAGIAYVFLMNTGVSRTLTNNRMFLROGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMRMVHSNLTFRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSLA 180
DB 121 LVIAVERHMSIMRMVHSNLTFRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSLA 180
QY 181 PIYSRSYLFWTVSNLMAFLIMVYVLLRIYYVKRTNVLSPHTSGSISRRTPPKLMKT 240
DB 181 PIYSRSYLFWTVSNLMAFLIMVYVLLRIYYVKRTNVLSPHTSGSISRRTPPKLMKT 240
QY 241 VMTVLGAFVVCWTPGLVLLPLDGLNCRQCGVOHVKRMFLALLNSVNPPIIYSKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVLLPLDGLNCRQCGVOHVKRMFLALLNSVNPPIIYSKDEDM 300
QY 301 YGTMKMKICFSQENPERPSPRIPTVLSRSDTSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKMKICFSQENPERPSPRIPTVLSRSDTSQYIEDSISOGAVCNKSTS 353

RESULT 10
US-10-228-762-2
;; Sequence 2, Application US/10228762
;; Publication No. US20030130493A1
;; GENERAL INFORMATION:
;; APPLICANT: Bonini, James A.
;; APPLICANT: Huang, Ling Yan
;; APPLICANT: Borowsky, Beth E.
;; APPLICANT: Salton, John A.
;; APPLICANT: Wilson, Amy
;; APPLICANT: Nagorny, Raisa
;; TITLE OF INVENTION: DNA Encoding Edg7 Receptor
;; FILE REFERENCE: 58230-a
;; CURRENT APPLICATION NUMBER: US/10/228,762
;; CURRENT FILING DATE: 2002-08-26
;; PRIOR APPLICATION NUMBER: US/09/356,315
;; PRIOR FILING DATE: 1999-07-19
;; PRIOR APPLICATION NUMBER: 09/253,998
;; PRIOR FILING DATE: 1999-02-22
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn Ver. 2.0 - beta
;; SEQ ID NO 2
;; LENGTH: 353
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-228-762-2

Query Match 99.5%; Score 1838; DB 16; Length 353;
Best Local Similarity 99.7%; Pred. No. 4e-170;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MNECHYKHMDFNRSNTDVTVDWMTGKLVILCVGTFECLFIFSSLSVIAAYTKRK 60

DB 1 MNECHYKHMDFNRSNTDVTVDWMTGKLVILCVGTFECLFIFSSLSVIAAYTKRK 60
QY 61 FHFFPYLLANLAADFFAGIAYVFLMNTGVSRTLTNNRMFLROGLDSSLTASLTNL 120
DB 61 FHFFPYLLANLAADFFAGIAYVFLMNTGVSRTLTNNRMFLROGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMRMVHSNLTFRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSLA 180
DB 121 LVIAVERHMSIMRMVHSNLTFRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSLA 180
QY 181 PIYSRSYLFWTVSNLMAFLIMVYVLLRIYYVKRTNVLSPHTSGSISRRTPPKLMKT 240
DB 181 PIYSRSYLFWTVSNLMAFLIMVYVLLRIYYVKRTNVLSPHTSGSISRRTPPKLMKT 240
QY 241 VMTVLGAFVVCWTPGLVLLPLDGLNCRQCGVOHVKRMFLALLNSVNPPIIYSKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVLLPLDGLNCRQCGVOHVKRMFLALLNSVNPPIIYSKDEDM 300
QY 301 YGTMKMKICFSQENPERPSPRIPTVLSRSDTSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKMKICFSQENPERPSPRIPTVLSRSDTSQYIEDSISOGAVCNKSTS 353

RESULT 11
US-09-879-225-2
;; Sequence 2, Application US/09879225
;; Patent No. US2002061558A1
;; GENERAL INFORMATION:
;; APPLICANT: LANE, Pamela
;; APPLICANT: TSUI, Ping
;; APPLICANT: ELISHOURBAGY, Nabila A.
;; TITLE OF INVENTION: MOUSE G PROTEIN COUPLED RECEPTOR EDG7
;; FILE REFERENCE: GP-70706
;; CURRENT APPLICATION NUMBER: US/09/879,225
;; CURRENT FILING DATE: 2001-06-12
;; PRIOR APPLICATION NUMBER: 60/210,926
;; PRIOR FILING DATE: 2000-06-12
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 354
;; TYPE: PRT
;; ORGANISM: MUS MUSCULUS
US-09-879-225-2

Query Match 91.6%; Score 1692.5; DB 9; Length 354;
Best Local Similarity 91.0%; Pred. No. 5.2e-156;
Matches 322; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

QY 1 MNECHYKHMDFNRSNTDVTVDWMTGKLVILCVGTFECLFIFSSLSVIAAYTKRK 60
DB 1 MNECHYKHMDFNRSNTDVTVDWMTGKLVILCVGTFECLFIFSSLSVIAAYTKRK 60
QY 61 FHFFPYLLANLAADFFAGIAYVFLMNTGVSRTLTNNRMFLROGLDSSLTASLTNL 120
DB 61 FHFFPYLLANLAADFFAGIAYVFLMNTGVSRTLTNNRMFLROGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMRMVHSNLTFRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSLA 180
DB 121 LVIAVERHMSIMRMVHSNLTFRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSLA 180
QY 181 PIYSRSYLFWTVSNLMAFLIMVYVLLRIYYVKRTNVLSPHTSGSISRRTPPKLMKT 240
DB 181 PIYSRSYLFWTVSNLMAFLIMVYVLLRIYYVKRTNVLSPHTSGSISRRTPPKLMKT 240
QY 241 VMTVLGAFVVCWTPGLVLLPLDGLNCRQCGVOHVKRMFLALLNSVNPPIIYSKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVLLPLDGLNCRQCGVOHVKRMFLALLNSVNPPIIYSKDEDM 300
QY 301 YGTMKMKICFSQENPERPSPRIPTVLSRSDTSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKMKICFSQENPERPSPRIPTVLSRSDTSQYIEDSISOGAVCNKSTS 353


```
RESULT 15
US-09-971-228-6
; Sequence 6, Application US/09971228
; Patent No. US2002015512A1
; GENERAL INFORMATION:
; APPLICANT: Liao, X. Charlene
; APPLICANT: Masuda, Etsedan
; APPLICANT: Chu, Peter
; APPLICANT: Pardo, Jorge
; APPLICANT: Li, Congfen
; APPLICANT: Zhao, Haoran
; APPLICANT: Jiang, Yingsheng
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration
; FILE REFERENCE: 021044-000310US
; CURRENT APPLICATION NUMBER: US/09/971,228
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/284,763
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human endothelial differentiation G-protein
; OTHER INFORMATION: coupled receptor (GPCR) 2 (EDG2)
US-09-971-228-6

Query Match      51.3%; Score 948.5; DB 10; Length 364;
Best Local Similarity 51.6%; Pred. No. 8.2e-84;
Matches 175; Conservative 76; Mismatches 75; Indels 13; Gaps 5;

QY      1 MNE--CHDKAMDPPYNSNDYVDDM-TGTRLVVLCVCGTFPCLFIFPSNSLYTAAYIK 57
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      19 MNEPQCFYNESIAFFYNSGRHLAENWTSKLVML--GITVCIFIMLANLVVAIYV 76
QY      58 NRRFHPFYLLANLAADFFAGIAYVFLMFNTGVSFSLVNRWFLRQGLDSSLTASL 117
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      77 NRRFHPFYLLANLAADFFAGIAYVFLMFNTGVSFSLVNRWFLRQGLDSSLTASV 136
QY      118 TNLVIAVERHMSIRMRHSNLTJRRVTLILVMAIAIFGAVPTLGMNCNISACS 177
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      137 ANLAIATERHITVFRMQLTRMSNRVYVIVITMAIYGAIPSYGMNCIDENCS 196
QY      178 SLAPYSRSYLVFTVSNLMAFLIMVVYVLRIVYVKKRNVLSPHTSGISRRRTPKL 237
      ::||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      197 NMAPLYSDSYLVFAIFMLVTFVWVLYAHIFGYRQTRMSRHSNGPRRRDYMMSL 256
QY      238 MKTVTVLGARVVCWTPGLVVLPLDGLNCRGCGVQVHRKRWFLLLALNSVNPITYSKD 297
      :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      257 LKTVIVYIGAFIICHTPGLVLLLD-VCCPQCDVLAERKFLLLAEFNSAMNPITYSRD 315
QY      298 EDNYGTMKRMICFESQENP-----ERRRSPSTVLS 329
      ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      316 KEMSATFRQILCCQCRSENPTGPTSSDRSASSINHTILA 354
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Search completed: August 18, 2003, 15:21:30

Job time : 58 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 14:32:44 ; Search time 23 Seconds

(without alignments)
721.758 Million cell updates/sec

Title: US-09-581-252-14

Perfect score: 1848
Sequence: 1 MNECHYKHMDFYRNSMTD.....GSQYIEDSIISGAVCNKSTS 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Optimal number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1838	99.5	353	1	EDG7_HUMAN
2	1697.5	91.9	354	1	EDG7_RAT
3	1692.5	91.6	354	1	EDG7_MOUSE
4	955.5	51.7	366	1	LP11_XENLA
5	948.5	51.3	364	1	EDG2_HUMAN
6	947.5	51.3	366	1	LP12_XENLA
7	946.5	51.2	364	1	EDG2_MOUSE
8	932.5	50.5	393	1	EDG2_SHEEP
9	929.5	50.3	364	1	EDG2_BOVIN
10	843.5	45.4	351	1	EDG4_HUMAN
11	839	45.4	351	1	EDG4_MACFA
12	736.5	39.9	348	1	EDG4_MOUSE
13	546	29.5	382	1	EDG1_MOUSE
14	541	29.3	383	1	EDG1_RAT
15	537	29.1	378	1	EDG3_HUMAN
16	533.5	28.9	381	1	EDG1_HUMAN
17	499	27.0	352	1	H218_RAT
18	352	19.0	330	1	GPR3_HUMAN
19	351	19.0	330	1	GPR3_MOUSE
20	347	18.8	472	1	CB1R_MOUSE
21	347	18.8	472	1	CB1R_FELCA
22	347	18.8	473	1	CB1R_MOUSE
23	344	18.6	473	1	CB1R_POEGU
24	344	18.6	473	1	CB1R_TARGR
25	341	18.5	472	1	CB1R_HUMAN
26	340	18.4	468	1	CB1A_FUGRU
27	334	18.1	325	1	MCSR_PANTR
28	329.5	17.8	334	1	GP12_HUMAN
29	328	17.7	325	1	MCSR_HUMAN
30	327.5	17.7	362	1	GPR6_HUMAN
31	326.5	17.7	334	1	GP12_MOUSE
32	326.5	17.7	334	1	GP12_RAT
33	326.5	17.7	363	1	GPR6_RAT

34	326	17.6	325	1	MCSR_MOUSE	P41149 mus musculu
35	319.5	17.3	332	1	MCSR_PIG	O97504 sus scrofa
36	318.5	17.2	470	1	CB1B_FUGRU	O98895 fugu rubrip
37	314.5	17.0	332	1	MCSR_HUMAN	P32245 homo sapien
38	314	17.0	325	1	MCSR_SHEEP	P41983 ovis aries
39	312	16.9	325	1	MCSR_RAT	P35345 ratu
40	310	16.8	325	1	MCSR_BOVIN	P56451 bos taurus
41	307.5	16.6	332	1	MCSR_BOVIN	P54118 bos taurus
42	302.5	16.4	180	1	EDG5_MOUSE	P52592 mus musculu
43	299.5	16.2	332	1	EDG5_MOUSE	P70596 ratu
44	295	16.0	332	1	MCSR_RAT	P33033 mus musculu
45	294	15.9	390	1	SH1B_HUMAN	P28222 homo sapien

ALIGNMENTS

RESULT 1
EDG7_HUMAN STANDARD; PRT; 353 AA.
AC 09UBV5;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lysophosphatidic acid receptor Edg-7 (LPA receptor 3) (LPA-3).
GN EDG7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-T-cell;
RX MEDLINE=99419064; PubMed=10488122;
RA Bando K., Aoki J., Hosono H., Kobayashi S., Kobayashi T.,
Muraikami-Murotoshi K., Tsujimoto M., Arai H., Inoue K.;
RT Molecular cloning and characterization of a novel human G-protein-
coupled receptor, EDG7, for lysophosphatidic acid.;
J. Biol. Chem. 274:27776-27785(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Embryonic Kidney;
RX MEDLINE=20193876; PubMed=10727522;
RA Im D.-S., Heise C.E., Harding M.A., George S.R., O'Dowd B.F.,
Theodorescu D., Lynch K.R.;
RT Molecular cloning and characterization of a lysophosphatidic acid
receptor, Edg-7, expressed in prostate.;
Mol. Pharmacol. 57:753-759(2000).
RN [3]
RP REVIEW.
RX MEDLINE=20545693; PubMed=11093753;
RA Contos J.J.A., Ishii I., Chun J.;
RT "Lysophosphatidic acid receptors";
Mol. Pharmacol. 58:1188-1196(2000).
CC -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of
diverse cellular activities. May play a role in the development of
ovarian cancer. Seems to be coupled to the G(i1)/G(o) and G(q)
families of heteromeric G proteins.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Most abundantly expressed in prostate, testes,
pancreas, and heart, with moderate levels in lung and ovary. No
detectable expression in brain, placenta, liver, skeletal muscle,
kidney, spleen, thymus, small intestine, colon, or peripheral
blood leukocytes.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----
DR EMBL; AF127138; AAD56311.1; -
DR EMBL; AF186380; AAF00530.1; -
DR Genew; HGNC:14298; EDG7.
DR MIM; 605106; -
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0008289; C: lipid binding activity; TAS.
DR GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0007187; P: G-protein signaling, coupled to cyclic nucl. . . ; TAS.
DR GO; GO:0007268; P: synaptic transmission; TAS.
DR InterPro; IPR005385; EDG7_receptor.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR InterPro; IPR004065; LPAR_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1560; EDG7RECEPTOR.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; LPARRECEPTOR.
DR PROSITE; PS50262; G_PROTEIN_REC_P1_1; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Lipoprotein; Palmitate.
DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
TRANSMEM 32 52 1 (POTENTIAL).
CYTOPLASMIC 53 67 CYTOPLASMIC (POTENTIAL).
TRANSMEM 68 88 2 (POTENTIAL).
DOMAIN 89 101 EXTRACELLULAR (POTENTIAL).
TRANSMEM 102 124 3 (POTENTIAL).
CYTOPLASMIC 125 146 CYTOPLASMIC (POTENTIAL).
TRANSMEM 147 167 4 (POTENTIAL).
DOMAIN 168 186 EXTRACELLULAR (POTENTIAL).
TRANSMEM 187 207 5 (POTENTIAL).
CYTOPLASMIC 208 240 CYTOPLASMIC (POTENTIAL).
TRANSMEM 241 261 6 (POTENTIAL).
DOMAIN 262 276 EXTRACELLULAR (POTENTIAL).
TRANSMEM 277 297 7 (POTENTIAL).
CYTOPLASMIC 298 353 CYTOPLASMIC (POTENTIAL).
DOMAIN 309 309 PALMITATE (BY SIMILARITY).
LIPID 15 15 N-LINKED (GLCNAC. . . ) (POTENTIAL).
CARBOHYD 172 172 N-LINKED (GLCNAC. . . ) (POTENTIAL).
SEQUENCE 353 AA; 40128 MM; 105DC9DD185E2CE7 CMC64;

Query Match 99.5%; Score 1838; DB 1; Length 353;
Best Local Similarity 99.7%; Pred. No. 5.4e-123;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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AC Q8K5ED; Q9ESJ6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lysophosphatidic acid receptor Edg-7 (LPA receptor 3) (LPA-3)
DE (smPCR32).
GN Edg7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Higashioaka M., Mori K.;
RT "Molecular cloning of the rat Edg7 protein and its identification as a
RL functional cellular receptor for lysophosphatidic acid.";
RN Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
CC [2]
CC SEQUENCE OF 8-354 FROM N.A.
CC STRAIN=Sprague-Dawley;
CC Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
RT "Identification and characterization of novel G-protein coupled
RL receptors expressed in regenerating peripheral nerve.";
CC Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of
CC diverse cellular activities. Seems to be coupled to the G(i)/G(o)
CC and G(q) families of heteromeric G proteins (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB051164; BAB91247.1; -
DR EMBL; AF097733; AAG24262.1; ALT INIT.
DR InterPro; IPR005385; EDG7_receptor.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR InterPro; IPR004065; LPAR_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1560; EDG7RECEPTOR.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PRINTS; PRO1527; LPARRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_REC_P2_1; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Phosphorylation; Lipoprotein; Palmitate.
DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
TRANSMEM 32 52 1 (POTENTIAL).
CYTOPLASMIC 53 67 CYTOPLASMIC (POTENTIAL).
TRANSMEM 68 88 2 (POTENTIAL).
DOMAIN 89 101 EXTRACELLULAR (POTENTIAL).
TRANSMEM 102 124 3 (POTENTIAL).
CYTOPLASMIC 125 146 CYTOPLASMIC (POTENTIAL).
TRANSMEM 147 167 4 (POTENTIAL).
DOMAIN 168 186 EXTRACELLULAR (POTENTIAL).
TRANSMEM 187 207 5 (POTENTIAL).
CYTOPLASMIC 208 240 CYTOPLASMIC (POTENTIAL).
TRANSMEM 241 261 6 (POTENTIAL).
DOMAIN 262 276 EXTRACELLULAR (POTENTIAL).
TRANSMEM 277 295 7 (POTENTIAL).
CYTOPLASMIC 296 354 CYTOPLASMIC (POTENTIAL).
LIPID 309 309 PALMITATE (BY SIMILARITY).
CARBOHYD 15 15 N-LINKED (GLCNAC. . . ) (POTENTIAL).
CONFLICT 172 172 N-LINKED (GLCNAC. . . ) (POTENTIAL).
SEQUENCE 354 AA; 40286 MM; 3536C8FA6EC59286 CMC64;

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Query Match 91.9%; Score 1697.5; DB 1; Length 354;
 Best Local Similarity 91.0%; Pred. No. 4.4e-113;
 Matches 322; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

QY 1 MNECHYDRHDFEYRNSNTDVTVDWGTGKLVIVLCVGFEECLIFPESNSLYIAAYTKRK 60
 DB 1 MNECHYDRHDFEYRNSNTDVTVDWGTGKLVIVLCVGFEECLIFPESNSLYIAAYTKRK 60
 QY 61 FHFFPYLLANLAAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLNL 120
 DB 61 FHFFPYLLANLAAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLNL 120
 QY 121 LVIAVERHMSIMRMVHNSLTKRKRTLILLYMAIAIFMGAVPTLGMNCLNISACSSLA 180
 DB 121 LVIAVERHMSIMRMVHNSLTKRKRTLILLYMAIAIFMGAVPTLGMNCLNISACSSLA 180
 QY 181 PIYSRSYLVEFTVSNLMAFLMNVVYLRLIYVYVKKRTNVLSPHTSGSISRRTPKLMKT 240
 DB 181 PIYSRSYLVEFTVSNLMAFLMNVVYLRLIYVYVKKRTNVLSPHTSGSISRRTPKLMKT 240
 QY 241 VMTVLGAFVVCWTPGLVYVLPDLGNCRCQGVQHVYKRWFLLLALLNSVNPPIIYSKDEDM 300
 DB 241 VMTVLGAFVVCWTPGLVYVLPDLGNCRCQGVQHVYKRWFLLLALLNSVNPPIIYSKDEDM 300
 QY 301 YGTMKMKICFSQSE-NPERRPSRIPSTVLSRDSQYIEDSISOGAVCNKSTS 353
 DB 301 YGTMKMKICFSQSE-NPERRPSRIPSTVLSRDSQYIEDSISOGAVCNKSTS 353

RESULT 3
 EDG7_MOUSE STANDARD; PRT; 354 AA.
 AC Q9EQJ3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lysophosphatidic acid receptor Edg-7 (LPA receptor 3) (LPA-3).
 GN Edg7 OR LPA3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ, and Swiss Webster / NIH;
 RX MEDLINE=21213908; PubMed=11313151;
 RA Cortos J.J.A., Chun J.;
 RT "The mouse lp(a3)/Edg7 lysophosphatidic acid receptor gene: genomic structure, chromosomal localization, and expression pattern.";
 LN Gene 267:243-253(2001).
 RN [2]
 RP ERRATUM.
 RA Cortos J.J.A., Chun J.;
 RL Gene 272:345-345(2001).
 CC -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of diverse cellular activities. Seems to be coupled to the G(1)/G(0) and G(q) families of heteromeric G proteins.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Most abundantly expressed in testes, kidney, in heart, stomach, spleen, and adult and perinatal brain. Little or no expression in embryonic brain, liver, or thymus.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; AF293845; AAG13674.1; .

DR EMBL; AF272365; AK02017.1; .
 DR EMBL; AF272364; AK02017.1; JOINED.
 DR MGD; MGI:1929469; Edg7.
 DR InterPro; IPR005385; Edg7_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR004065; LPAreceptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01560; EDG7RECEPTOR.
 DR PRINTS; PR02337; GPCR_RHODOPSIN.
 DR PRINTS; PR01527; LPAARECEPTOR.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_REC_P2_1; 1.
 DR KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 DR MultiGene family; Lipoprotein; Palmitate.
 FT DOMAIN 1 31
 FT TRANSMEM 32 52 1 (POTENTIAL).
 FT TRANSMEM 53 67 2 (POTENTIAL).
 FT TRANSMEM 68 88 3 (POTENTIAL).
 FT TRANSMEM 89 101 4 (POTENTIAL).
 FT TRANSMEM 102 124 5 (POTENTIAL).
 FT TRANSMEM 125 146 6 (POTENTIAL).
 FT TRANSMEM 147 167 7 (POTENTIAL).
 FT TRANSMEM 168 186 8 (POTENTIAL).
 FT TRANSMEM 187 207 9 (POTENTIAL).
 FT TRANSMEM 208 240 10 (POTENTIAL).
 FT TRANSMEM 241 261 11 (POTENTIAL).
 FT TRANSMEM 262 276 12 (POTENTIAL).
 FT TRANSMEM 277 295 13 (POTENTIAL).
 FT TRANSMEM 296 354 14 (POTENTIAL).
 FT DOMAIN 309 309 15 (POTENTIAL).
 FT CARBOHYD 15 15 16 (POTENTIAL).
 FT CARBOHYD 172 172 17 (POTENTIAL).
 SQ SEQUENCE 354 AA; 40315 MW; 8B6F9A3CA9C1F062 CRC64;

Query Match 91.6%; Score 1692.5; DB 1; Length 354;
 Best Local Similarity 91.0%; Pred. No. 9.9e-113;
 Matches 322; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

QY 1 MNECHYDRHDFEYRNSNTDVTVDWGTGKLVIVLCVGFEECLIFPESNSLYIAAYTKRK 60
 DB 1 MNECHYDRHDFEYRNSNTDVTVDWGTGKLVIVLCVGFEECLIFPESNSLYIAAYTKRK 60
 QY 61 FHFFPYLLANLAAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLNL 120
 DB 61 FHFFPYLLANLAAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLNL 120
 QY 121 LVIAVERHMSIMRMVHNSLTKRKRTLILLYMAIAIFMGAVPTLGMNCLNISACSSLA 180
 DB 121 LVIAVERHMSIMRMVHNSLTKRKRTLILLYMAIAIFMGAVPTLGMNCLNISACSSLA 180
 QY 181 PIYSRSYLVEFTVSNLMAFLMNVVYLRLIYVYVKKRTNVLSPHTSGSISRRTPKLMKT 240
 DB 181 PIYSRSYLVEFTVSNLMAFLMNVVYLRLIYVYVKKRTNVLSPHTSGSISRRTPKLMKT 240
 QY 241 VMTVLGAFVVCWTPGLVYVLPDLGNCRCQGVQHVYKRWFLLLALLNSVNPPIIYSKDEDM 300
 DB 241 VMTVLGAFVVCWTPGLVYVLPDLGNCRCQGVQHVYKRWFLLLALLNSVNPPIIYSKDEDM 300
 QY 301 YGTMKMKICFSQSE-NPERRPSRIPSTVLSRDSQYIEDSISOGAVCNKSTS 353
 DB 301 YGTMKMKICFSQSE-NPERRPSRIPSTVLSRDSQYIEDSISOGAVCNKSTS 353

RESULT 4
 LP11_XENLA STANDARD; PRT; 366 AA.
 AC Q9P017;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lysophosphatidic acid receptor LPA1 homolog 1 (xLPA1-1).
 GN LPA1R1 OR LPA1R.
 OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus.
 NC NCBI_TaxID=8355;
 [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21226767; PubMed=11278944;
 RA Kimura Y., Schmitt A., Fukushima N., Ishii I., Kimura H.,
 RA Nedreda A.R., Chun J.;
 RT "Two novel Xenopus homologs of mammalian LPA1/EDG-2 function as
 RT lysophosphatidic acid receptors in Xenopus oocytes and mammalian
 RT cells";
 RL J. Biol. Chem. 276:15208-15215(2001).
 CC -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of
 CC diverse cellular activities. Probably coupled to the activation of
 CC the G(q) type of heteromeric G proteins, which activates the
 CC phospholipase C mediated signaling cascade.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed at high levels in oocytes and at
 CC lower levels in brain and spinal cord. Below detection level in
 CC lung, heart, kidney, liver, muscle, stomach, and intestine.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AJ249843; CAB62282.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR004065; LPAR_receptor.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PRINTS: PR01527; LPAR_RECEPTOR.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Lipoprotein; Palmitate.
 FT DOMAIN 1 55
 FT TRANSSEM 56 76
 FT DOMAIN 77 88
 FT TRANSSEM 89 109
 FT DOMAIN 110 122
 FT TRANSSEM 123 145
 FT DOMAIN 146 165
 FT TRANSSEM 166 186
 FT DOMAIN 187 207
 FT TRANSSEM 208 228
 FT DOMAIN 229 261
 FT TRANSSEM 262 282
 FT DOMAIN 283 290
 FT TRANSSEM 291 313
 FT DOMAIN 314 366
 FT TRANSSEM 329 329
 FT LIPID 329 329
 FT CARBOHYD 29 29
 FT CARBOHYD 37 37
 FT SEQUENCE 366 AA; 41363 MW; 2F5661BD13DCABE CRC64;
 SO
 Query Match 51.78; Score 955.5; DB 1; Length 366;
 Best Local Similarity 51.28; Pred. No. 1e-60;
 Matches 172; Conservative 79; Mismatches 74; Indels 11; Gaps 4;
 OY 2 NECHYDHDHDFNRSNTDVTVDWGTG-TKLYIVICVTEFFCLTFEFSNSIVIAVITNRK 60
 DB 24 SCQYVNTTIAFFNRSKYATLATEMNAVSKLWGL--GIYICIFMLANLMLVMAIYVNR 81
 OY 61 FHPFPYLLANLAADFPAGIAVYFLMNTGPKVSKTLTVNRWFLROGLDLSLSTASTNL 120
 DB 82 FHPFPYLLANLAADFPAGIAVYFLMNTGPKVSKTLTVNRWFLROGLDLSLSTASTNL 141

OY 121 LVIAVERHMSIMRNRVSNLTKKKRYTLLILMLMAIAFMGAVPTLGNVCLNISACSSLA 180
 DB 142 LAIAIERHITVEFRQGLTRMSRRVYIVYIVMFAIYMGAIIPVGNVICIDLEQCSMA 201
 OY 181 PIYRSIVLWTVSNLMAFLIMVYVYIRIYVYVYKRNIVLSPHSGISRRRTPKMLKT 240
 DB 202 PLYSDSYLIEFTITNLVTFVMAVYIAHIFVYVYKQKRMKSRHSSGGRNDDTMSDLKT 261
 OY 241 VMTVLGAFVVCVGTGLVPLPDGLNCRCQGQVHQHAKRNFLLALNLSVNPITYSKDEM 300
 DB 262 VVIYLGAFVYCVMTGLVILLID-ICPCCNILAEKFFLLAEKNSANPLITYSRDEM 320
 OY 301 YGTMKMICFSQEN-----PERRPSRIPSTYLS 329
 DB 321 SATFKQLICQRTENVNGPTEGSDRSASLWHTILA 356
 RESULT 5
 EDG2_HUMAN STANDARD; PRT; 364 AA.
 AC 092633; 000656; 000722; P78351;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 26-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Lysophosphatidic acid receptor Edg-2 (LPA receptor 1) (LPA-1).
 GN EDG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97224397; PubMed=9070858;
 RA An S., Dickens M.A., Bleu T., Hallmark O.G., Goetzl E.J.;
 RT "Molecular cloning of the human Edg2 protein and its identification
 RT as a functional cellular receptor for lysophosphatidic acid";
 RL Biochem. Biophys. Res. Commun. 231:619-622(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97224241; PubMed=9069262;
 RA Moolenaar W.H., Krenenburg O., Postma F.R., Zondag G.C.M.;
 RT "Lysophosphatidic acid: G-protein signalling and cellular responses";
 RL Curr. Opin. Cell Biol. 9:168-173(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RT TISSUE=Hippocampus, and Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gundaratne P.R.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan M., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP REVIEW.
 RX MEDLINE=20545693; PubMed=11093753;
 RA Contos J.J.A., Ishii I., Chun J.;
 RT "Lysophosphatidic acid receptors";
 RL Mol. Pharmacol. 58:1188-1196(2000).

CC cells of the peripheral nervous system. Expressed in many other
 CC tissues, including testes, lung, heart, intestine, spleen, kidney,
 CC thymus, and stomach. No expression in liver.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: U70622; AAC52923.1; -
 DR EMBL: U48235; AAC53035.1; -
 DR EMBL: AF075456; AAC34301.1; -
 DR EMBL: AF075453; AAC34301.1; JOINED.
 DR EMBL: AF075455; AAC34301.1; JOINED.
 DR EMBL: AF075456; AAC34302.1; -
 DR EMBL: BC025425; AAC34302.1; JOINED.
 DR EMBL: AF014418; AAB86381.1; -
 DR EMBL: AF090347; AAG24469.1; -
 DR MGD: MGI:108429; Edg2.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR004065; LPARreceptor.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_REC_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_REC_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Lipoprotein; Palmitate; Alternative splicing.
 FT DOMAIN 1 50
 FT TRANSMEM 51 75
 FT DOMAIN 76 82
 FT TRANSMEM 83 111
 FT DOMAIN 112 125
 FT TRANSMEM 126 144
 FT DOMAIN 145 163
 FT TRANSMEM 164 189
 FT DOMAIN 190 205
 FT TRANSMEM 206 226
 FT DOMAIN 227 258
 FT TRANSMEM 259 280
 FT DOMAIN 281 294
 FT TRANSMEM 295 315
 FT DOMAIN 316 364
 FT LIPID 327 327
 FT CARBOHYD 27 27
 FT CARBOHYD 35 35
 FT VARSPLIC 1 18
 FT CONFLICT 119 119
 FT CONFLICT 181 183
 FT CONFLICT 225 225
 SQ SEQUENCE 364 AA; 41119 MW; B0FA6265A688B7 CRC64;
 Query Match 51.2%; Score 946.5; DB 1; Length 364;
 Best Local Similarity 51.9%; Pred. No. 4,4e-60;
 Matches 176; Conservative 75; Mismatches 75; Indels 13; Gaps 5;
 QY 1 MNE--CHYDKHMDFFYNSNEDTVDM--TGTKLIVLVLCGTFEFLFSPFSNLTAAVTK 57
 DB 19 MNEOCFFYNESIAFYNSGKILATEENTVSKLVGL--GIVCYFIAMLANLVAIV 76
 QY 58 NKRHFPPYLIANLAADDFAGIAYVFLMFTGVSFKTLVNVNRFLOGLLDSSLTASL 117
 DB 77 NKRHFPPYLIANLAADDFAGIAYVFLMFTGVSFKTLVNVNRFLOGLLDSSLTASV 136
 QY 118 TNLVIAVERHMSIMRMVHSLTKKRYTLILLWMAIAPFGAVPTGLMNCISACS 177
 DB 137 ANLAIATERHTVERMQLHTMSNRVVVIVLWMAIAGALPSVGMNCICIDHCS 196

QY 178 SLAPIRSYLVFWTNSMLAPLIMVYVYKRTNVLSPHTSGISRRRTPMKL 237
 DB 197 NMAPLXDSYLVFWTNSMLAPLIMVYVYKRTNVLSPHTSGISRRRTPMKL 256
 QY 238 KRTVTVIGAFVYVWTPGLVPLDGLNCRQGVQVHKRMFLALLNSVNPITYSKD 297
 DB 257 LKTVVTVIGAFVYVWTPGLVPLDGLNCRQGVQVHKRMFLALLNSVNPITYSKD 315
 QY 298 EDMGTMKMKICFSGQENP-----ERRSPITPTVLS 329
 DB 316 KEMSAFPQIILCCQRRNENPTEGSDNSASSLNTHTLA 354
 RESULT 8
 ID EDG2_SHEEP STANDARD; PRT; 393 AA.
 AC P46628;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lysophosphatidic acid receptor Edg-2 (Lpa receptor 1) (Lpa-1).
 GN EDG2 OR EDG-2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=plutitary pars tuberalis;
 RX MEDLINE=96430916; PubMed=8833998;
 RA Masana M.I., Brown R.C., Pu H., Gurney M.E., Dubocovich M.L.;
 RT Cloning and characterization of a new member of the G-protein
 RT coupled receptor EDG family".
 RL Recept. Channels 3:255-262(1995).
 CC -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of
 CC diverse cellular activities. Seems to be coupled to the G(11)/G(0),
 CC G(12)/G(13), and G(4) families of heteromeric G proteins (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@sdb-sdb.ch).
 CC -----
 DR EMBL: U18405; AAB52368.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR004065; LPARreceptor.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PRINTS: PR01527; LPARRECEPTOR.
 DR PROSITE: PS00237; G_PROTEIN_REC_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_REC_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Lipoprotein; Palmitate.
 FT DOMAIN 1 50
 FT TRANSMEM 51 75
 FT DOMAIN 76 82
 FT TRANSMEM 83 111
 FT DOMAIN 112 125
 FT TRANSMEM 126 144
 FT DOMAIN 145 163
 FT TRANSMEM 164 189
 FT DOMAIN 190 205
 FT TRANSMEM 206 226
 FT DOMAIN 227 258
 FT TRANSMEM 259 280

FT	DOMAIN	281	294	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	295	315	7 (POTENTIAL).
FT	DOMAIN	316	393	CYTOPLASMIC (POTENTIAL).
FT	LIPID	327	327	PALMITATE (BY SIMILARITY).
FT	CARBOHYD	27	27	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	35	35	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	393 AA;	44433 MM;	356E961153C345FC CRC64;
Query Match				
Best Local Similarity		50.5%;	Score 932.5;	DB 1; Length 393;
Matches 172;		Conservative 78;	Mismatches 76;	Indels 13; Gaps 5;
QY	1 MNE--CHYDKHMEFFYNSNTDVTDDW-TGKTLVILVCGTFPLETFEFSNLSIAVTK 57			
Db	19 MNEQCFNEISIAFFYNSRGKYLATEWNTVSKLWGL--GITVCFILMLNLVVAITY 76			
QY	58 NRKHFFPYVYLALMLAADFAGIAYVFLMNTGVSSTLTVNMFPLROGLDSSIRASL 117			
Db	77 NRHFHFFIYVLMNLAAADFPAGIAYVFLMNTGPNTRRLRLRLQGLIDTVYASV 136			
QY	118 TNLVIVVERHMSIMRMRHSHNLKKRPTLLILVMAIAPMAGVPTLGMNCLNISACS 177			
Db	137 ANLAIAMERIIITYFRQGLHTRMSNRVYVIVIMYALMGALPSYGNACIDIEGCS 196			
QY	178 SLAFIYSRYVETVSNLMAPLIMVYVYLIYVYKKNIVLSPHISGISRRTPKTL 237			
Db	197 NMALPYSYSYLVFAIFNLVTFVVMVLYAHIFGVYRQFTRMSHSGSPRRNDTMSL 256			
QY	238 MKYTVIVGAFVVCMTPLVYLPLDGLMCRQCGVOHYHWRWPLLLALNSVYNPITYSKD 297			
Db	257 LKTVIVYVGNATICTPGLVYLLLD-VCCPCQDVLATKEFLLLAERFSANMPITYSRD 315			
QY	298 EDMTGYMKMKTCFSQEN-----PERRPSRIDSTVLS 329			
Db	316 KEMSATFROILCCORSENTSGPTGSDRSASSLNHTILA 354			
RESULT 9				
EDG2_BOVIN				
ID	EDG2_BOVIN	STANDARD;	PRT;	364 AA.
AC	Q28031;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Lysophosphatidic acid receptor Edg-2 (LPA receptor 1) (LPA-1)			
DE	(Recl.3).			
GN	Edg2.			
OS	Bos taurus (Bovine).			
RP	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
RP	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
RP	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Brain;			
RX	MEDLINE=97165887; PubMed=9013780;			
RA	Macrae A.D., Piemont R.T., Jaber M., Petersen A.S., Iefkowitz R.J.;			
RA	"Cloning, characterization, and chromosomal localization of recl.3, a			
RA	member of the G-protein-coupled receptor family highly expressed in			
RA	brain. "			
RL	Brain Res. Mol. Brain Res. 42:245-254(1996).			
CC	-1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of			
CC	diverse cellular activities. Seems to be coupled to the G(i)/G(0),			
CC	G(i2)/G(i3), and G(q) families of heteromeric G proteins (by			
CC	similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			

[illegible]

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A., AND VARIANT OVARIAN CARCINOMA.
 RC TISSUE-Ovarian carcinoma;
 RX MEDLINE=98192573; PubMed=9525886;
 RA An S., Bieu T., Hallmark O.G., Goetzl E.J.;
 RT "Characterization of a novel subtype of human G protein-coupled
 RL receptor for lysophosphatidic acid.";
 RN J. Biol. Chem. 273:7906-7910(1998).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20382744; PubMed=10922489;
 RA Bandoh K., Aoki J., Taira A., Tsujimoto M., Arai H., Inoue K.;
 RT "Lysophosphatidic acid (LPA) receptors of the EDG family are
 RL differentially activated by LPA species. Structure-activity
 RN relationship of cloned LPA receptors.";
 RP FEBS Lett. 478:159-165(2000).
 [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Colon cancer;
 RA An S.;
 RT "Human Edg4 lysophosphatidic acid receptor cDNA encoding a putative
 RL protein with COOH-terminus different from the previously-reported
 RN Edg4.";
 RP Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCreedy P.M., Adamson A.W., Burkhart-Schultz K.,
 RA Garcia E., Kyle A., Ramirez M., Stillwagen S., Garness J., Dangman L.,
 RA Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
 RA Carrano A.V.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Lung;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stopleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udels T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.T., Skalski U., Smalios D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RP REVIEW.
 RX MEDLINE=20545693; PubMed=11093753;
 RA Contos J.J.A., Ishii I., Chun J.;
 RT "Lysophosphatidic acid receptors.";
 RN Mol. Pharmacol. 58:1188-1196(2000).
 [7]
 RP IDENTIFICATION OF A PROBABLE FRAMESHIFT MUTATION.
 RX MEDLINE=20195626; PubMed=10729222;
 RA Contos J.J.A., Chun J.;
 RT "Genomic characterization of the lysophosphatidic acid receptor gene,
 RL lp(2)(2)/Edg4, and identification of a frameshift mutation in a
 CC previously characterized cDNA.";
 CC Genomics 64:155-169(2000).
 CC -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of
 CC diverse cellular activities. Seems to be coupled to the G(1)/G(0),

CC G(12)/G(13), and G(q) families of heteromeric G proteins.
 CC SUBCELLULAR LOCATION: Integral membrane protein.
 CC TISSUE SPECIFICITY: Expressed most abundantly in testes and
 CC peripheral blood leukocytes with less expression in pancreas,
 CC spleen, thymus and prostate. Little or no expression in heart,
 CC brain, placenta, lung, liver, skeletal muscle, kidney, ovary,
 CC small intestine, or colon.
 CC MISCELLANEOUS: Ref.1 cDNA clone has a guanine nucleotide deletion
 CC that causes a frameshift near its C-terminal coding region. This
 CC likely reflects a somatic mutation in the ovary tumor cells from
 CC which the cDNA was isolated and may have altered the function of
 CC the encoded receptor, and contributed to transformation
 CC of the original ovary cells that formed a tumor.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: AF011466; AAC27728.1; ALT_FRAME.
 CC EMBL: AF233092; AAF43409.1; -.
 CC EMBL: AF197929; AAG28521.1; -.
 CC EMBL: AC002306; AAB61528.1; -.
 CC EMBL: BC025695; AAB25695.1; -.
 CC Genes: HGNC:3168; EDG4.
 CC MIM: 605110; -.
 CC InterPro: IPR004066; EDG4receptor.
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC InterPro: IPR004065; LPAreceptor.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS: PRO1528; EDG4RECEPTOR.
 CC PRINTS: PRO1527; GPCR RHODOPSN.
 CC PRINTS: PRO1527; LPA RECEPTOR.
 CC PROSITE: PS00237; G-PROTEIN_RECEP_FL1; 1.
 CC PROSITE: PS50262; G-PROTEIN_RECEP_FL2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Multigene family; Lipoprotein; Palmitate.
 CC DOMAIN 1 33
 CC TRANSMEM 34 54
 CC DOMAIN 55 69
 CC TRANSMEM 70 90
 CC DOMAIN 91 103
 CC TRANSMEM 104 126
 CC DOMAIN 127 146
 CC TRANSMEM 147 167
 CC DOMAIN 168 188
 CC TRANSMEM 189 209
 CC DOMAIN 210 242
 CC TRANSMEM 243 263
 CC DOMAIN 264 279
 CC TRANSMEM 280 297
 CC DOMAIN 298 351
 CC LIPID 311 311
 CC CARBOHYD 10 10
 CC CARBOHYD 18 18
 CC CONFLICT 221 221
 CC SEQUENCE 351 AA; 39084 MW; DE225B0B3B9351B8 CRC64;
 R -> S (IN REF. 3).
 N-LINKED (GLCNAC...) (POTENTIAL).
 N-LINKED (GLCNAC...) (POTENTIAL).
 Query Match 45.6%; Score 843.5; DB 1; Length 351;
 Best Local Similarity 50.3%; Pred No. 86-53;
 Matches 156; Conservative 60; Mismatches 93; Indels 1; Gaps 1;
 OY 1 MNECHYDKHMDPEFNNSNTDVTGTLVIVLCVGFPCFLFFFSNSLVAIAVKNRK 60
 DB 4 MCGCYNNEDTGFYNNNSGKELSHMR-PDVYVVALGLVSVYLVLTNLVLAALASNR 62
 OY 61 FHFFPYTLLANLAADDFAGIAYVFLMTGVSSTLYVNRNPLRGLDSSLSLNL 120
 DB 63 FHQPTYYLLGNLAADLFAVAVYLFPLMFTGRTARLSLGEVFLRGLDLSLTFASVATL 122

CC and embryonic brain. Other organs also express the transcript,
 CC including heart, lung, spleen, thymus, stomach, and adult brain.
 CC Several have little or no expression, including liver, small
 CC intestine, and skeletal muscle.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL: AF218844; AAF65684.1; -
 CC MGD: MGI:1858422; Edg4.
 CC InterPro: IPR004066; GPCR_Rhodopsin.
 CC InterPro: IPR004065; GPCR_Rhodopsin.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS: PR01528; EDG4RECEPTOR.
 CC PRINTS: PR00237; GPCR_Rhodopsin.
 CC PRINTS: PR01527; LPARRECEPTOR.
 CC PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
 CC PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Multigene family; Lipoprotein; Palmitate.
 CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 51 51 1 (POTENTIAL).
 CC TRANSMEM 52 66 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 67 87 2 (POTENTIAL).
 CC TRANSMEM 88 104 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 105 124 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 125 144 4 (POTENTIAL).
 CC TRANSMEM 145 165 4 (POTENTIAL).
 CC TRANSMEM 166 185 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 186 206 5 (POTENTIAL).
 CC TRANSMEM 207 239 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 240 260 6 (POTENTIAL).
 CC TRANSMEM 261 291 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 271 290 7 (POTENTIAL).
 CC DOMAIN 292 348 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 308 308 PALMITATE (BY SIMILARITY).
 CC TRANSMEM 7 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 348 AA; 38776 MW; E3594382D616052C CRC64;
 CC -----
 CC Query Match 39.9%; Score 736.5; DB 1; Length 348;
 CC Best Local Similarity 42.6%; Freq. No. 2.8e-45;
 CC Matches 147; Conservative 68; Mismatches 105; Indels 25; Gaps 4;
 CC -----
 CC 1 MNECHYDHMDFFVRSNTDVTGDKLVIVLCVGFCELFIFESNSIVAIYKRRK 60
 CC 1 GGCCTYNTTIGFFNNKSKELSHRR-PKDYVVAALGLTVSLVALLMLVIAALASNR 59
 CC 1 FHFPFYLLANLAADFFAGIAYVFLMNTGSPVSKTLVKNMFLROGLD----- 110
 CC 60 FHOPFYLLGNLAADDFAGMAYLFEMHTGP-----PHOALHQRILVATGPAHQPH 113
 CC 111 --SILFASLNLVIAVERHMSIMARVHSNLTKKRVTLLILVAIAIFGAVFTLGMN 168
 CC 114 GVSCHTAG-----IAVERHRSVAVVOLHSRLPRGRVYTLIVGWAALIGLILPAHWH 167
 CC 169 CLCNISACSLAPISRSYLVFMYNSLMAFLIMVYVYLYVYVYKRTNVLSPITSGSI 228
 CC 168 CLCIDDSGRVPLFSRSYLLAVALSLVFLVLAAYVTRIFFYKRRVERAEVNSCHP 227
 CC 229 SRRRTPMKMTVMTVIGAFVVCWTPGLVVLPLDGLNRCOGVOYHVKRMFTLLALNSV 288
 CC 228 RYRETTLSLVKTVVYIIIGAFVVCWTPGOVVLIDGLDKCTCNVLAVERKFTLLANSLV 287
 CC 289 NPILSYDEDMYGMKMKMCCFSGDENRRPRSRIPSTVLSRSDT 333
 CC -----

DB 288 NAVVYSCRDAMERTFRLLCCMCLRWSSHSARSASATGAST 332
 RESULT 13
 EDGL_MOUSE STANDARD: PRT; 382 AA.
 AC 008530;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-1998 (Rel. 36, Last annotation update)
 DE Probable G protein-coupled receptor EDG-1.
 GN EDG1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/c; TISSUE=liver;
 RX MEDLINE=97369927; PubMed=9226368;
 RA Liu C.H., Hla T.;
 RT "The mouse gene for the inducible G-protein-coupled receptor edg-1.";
 RL Genomics 43:15-24(1997).
 CC -1- FUNCTION: THIS INDUCIBLE EPITHELIAL CELL G-PROTEIN-COUPLED
 CC RECEPTOR MAY BE INVOLVED IN THE PROCESSES THAT REGULATE THE
 CC DIFFERENTIATION OF ENDOTHELIAL CELLS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES
 CC WITH HIGHEST LEVELS IN BRAIN, SPLEEN AND HEART. LOWER LEVELS
 CC FOUND IN LUNG, PLACENTA, MUSCLE, LIVER, UTERUS AND KIDNEY. VERY
 CC LOW LEVELS IN TESTIS AND THYMUS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL: U40811; AAC53294.1; -
 CC MGD: MGI:1096355; Edg1.
 CC GO: GO:0007193; P:G-protein signaling, adenylate cyclase inh. . .; IDA.
 CC InterPro: IPR000276; GPCR_Rhodopsin.
 CC InterPro: IPR004061; S1PReceptor.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCR_Rhodopsin.
 CC PRINTS: PR01523; S1PReceptor.
 CC PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 CC PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Phosphorylation; Lipoprotein; Palmitate.
 CC DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 47 71 1 (POTENTIAL).
 CC TRANSMEM 72 78 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 79 107 2 (POTENTIAL).
 CC TRANSMEM 108 121 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 122 140 3 (POTENTIAL).
 CC TRANSMEM 141 159 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 160 185 4 (POTENTIAL).
 CC TRANSMEM 186 201 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 202 222 5 (POTENTIAL).
 CC TRANSMEM 223 256 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 257 278 6 (POTENTIAL).
 CC TRANSMEM 279 294 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 295 315 7 (POTENTIAL).
 CC TRANSMEM 316 382 CYTOPLASMIC (POTENTIAL).
 CC CARBOHD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC LIPID 328 328 PALMITATE (BY SIMILARITY).
 CC MOD_RES 353 353 PHOSPHORYLATION (POTENTIAL).
 CC SEQUENCE 382 AA; 42571 MW; A0048993491C8957 CRC64;
 CC -----

Query Match 29.58; Score 546; DB 1; Length 382;
 Best Local Similarity 34.18; Pred. No. 8.5e-32;
 Matches 117; Conservative 79; Mismatches 125; Indels 22; Gaps 8;

27 GFKLVYLCVGFTEFCLEFFNSLYIAVKNRHPPEFYLLANLAADFPFGIAVFL 86
 44 GIKLTSVFT--LICCTIIENIEFVLTITKTKFHPMTYFGNLSLSDLAGVAATAN 101
 87 MENTGPVSKTLTVNRFLRGLDSSLTASLTNLVAVRHMSIMRVRHSLTKRVT 146
 102 LILSGATYKLTPOAWFLREGSMFVALASVSLAIIRYITLTKMKLHNSNSRSF 161
 147 LLLILWALIFPGAVPTLWNCICINISACSLAPIYSRYLVFWTVSNIMAFIIMVY 206
 162 LILSACWVSLILIGGLPSMGNCISSLSCSTVLPYHKHYIIFCTVFTLLLSIALLY 221
 207 LRIYVYKRTKNTVLSPI--TSGSISRRTPMKLMKTVMTVLGAFVVCWTPGLVPLD- 262
 222 CRISLVTRSRRLTRFKNISKRSRSEKS-LALIKTVIIVLSVFIACMAPFLILLDY 280
 263 LINCRCQGVQVHRWFLALLALNSVNPPIIYSYKDEDMYGMKMICFSQENPE---- 317
 281 GCAKACDILYKAEFLVALVNSGTNPILYITLTKEMRAFIIRIVSCCKCPNDSDAKRF 340

318 RRSRIPSTVLSR--SPTGSOYIEDS-----ISQAVCNKS 351
 341 KRP1-IPGMEFSRKSNDSSHPQKDDGNDPETIMSSGNVSSS 382

RESULT 14
 EDG1_RAT STANDARD; PRT; 383 AA.

AC P48303;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-1998 (Rel. 36, Last annotation update)
 DE Probable G protein-coupled receptor EDG-1.
 GN EDG1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum;
 RX MEDLINE=95047498; PubMed=7959012;
 RA Lado D.C., Browe C.S., Gaekin A.A., Borden J.M., MacLennan A.J.;
 RT "Cloning of the rat edg-1 immediate-early gene: expression pattern
 suggests diverse functions.";
 Gene 149:331-336(1994).
 -1- FUNCTION: IT IS POSSIBLE THAT IT ACTS AS A RECEPTOR FOR A TROPHIC
 FACTOR AND IS INVOLVED IN THE SURVIVAL OF BRAIN CELLS.
 -1- SUBCELLULAR LOCATION: Integral membrane protein.
 -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT EMBRYONIC DAY 15, AT
 POSTNATAL DAY 14 DETECTED IN SKIN, SPLEEN, LIVER, KIDNEY, HEART,
 TESTICLE, LUNG AND BRAIN. AT ADULTHOOD IS MOST ABUNDANT IN BRAIN.
 -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@sib-sib.ch).
 CC EMBL: U10303; AAA83418.1; -
 DR PUR: I53870; I53870.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR InterPro: IPR004061; S1PReceptor.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PRINTS: PR01523; S1PReceptor.

DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 47
 FT TRANSSEM 48 72
 FT DOMAIN 73 79
 FT TRANSSEM 80 108
 FT DOMAIN 109 122
 FT TRANSSEM 123 141
 FT DOMAIN 142 160
 FT TRANSSEM 161 186
 FT DOMAIN 187 202
 FT TRANSSEM 203 223
 FT DOMAIN 224 257
 FT TRANSSEM 258 279
 FT DOMAIN 280 295
 FT TRANSSEM 296 316
 FT DOMAIN 317 383
 FT CARBOHYD 31 31
 FT LIPID 329 329
 FT MOD_RES 354 354
 SQ SEQUENCE 383 AA; 42745 MM; 090BA6AE0DB4F3 CRC64;

Query Match 29.38; Score 541; DB 1; Length 383;
 Best Local Similarity 34.28; Pred. No. 1.9e-31;
 Matches 117; Conservative 77; Mismatches 128; Indels 20; Gaps 7;

27 GFKLVYLCVGFTEFCLEFFNSLYIAVKNRHPPEFYLLANLAADFPFGIAVFL 86
 45 GIKLTSVFT--LICCTIIENIEFVLTITKTKFHPMTYFGNLSLSDLAGVAATAN 102
 87 MENTGPVSKTLTVNRFLRGLDSSLTASLTNLVAVRHMSIMRVRHSLTKRVT 146
 103 LILSGATYKLTPOAWFLREGSMFVALASVSLAIIRYITLTKMKLHNSNSRSF 162
 147 LLLILWALIFPGAVPTLWNCICINISACSLAPIYSRYLVFWTVSNIMAFIIMVY 206
 163 LILSACWVSLILIGGLPSMGNCISSLSCSTVLPYHKHYIIFCTVFTLLLSIALLY 222
 207 LRIYVYKRTKNTVLSPI--TSGSISRRTPMKLMKTVMTVLGAFVVCWTPGLVPLD- 263
 223 CRISLVTRSRRLTRFKNISKRSRSEKS-LALIKTVIIVLSVFIACMAPFLILLDVG 282
 264 LINCRCQGVQVHRWFLALLALNSVNPPIIYSYKDEDMYGMKMICFSQENPE----R 318
 283 CKAKTODILYKAEFLVALVNSGTNPILYITLTKEMRAFIIRIVSCCKCPNDSDAKRF 342
 319 RPSRIPSTVLSR--SPTGSOYIEDS-----ISQAVCNKS 351
 343 RPI-IPGMEFSRKSNDSSHPQKDDGNDPETIMSSGNVSSS 383

RESULT 15
 EDG3_HUMAN STANDARD; PRT; 378 AA.

AC Q99500;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lysophospholipid receptor (EDG-3).
 GN EDG3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97032811; PubMed=8878560;
 RA Yamauchi F., Tokuda M., Hatake O., Brenner S.;
 RT "Molecular cloning of the novel human G protein-coupled receptor
 (GPCR) gene mapped on chromosome 9.";

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